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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:50:20 ; Search time 7570.62 Seconds
(without alignment)
10778.327 Million cell updates/sec

Title: US-10-085-233B-1

Perfect score: 1684
Sequence: 1 tcgcagcgtgacacacattt.....ctatgatgcatgacgagcg 1684

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl1:*
1: gb ba:*
2: gb heg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472.6	87.4	2525	6	AX147836 Sequence
2	1472.6	87.4	2525	6	AX521885 Sequence
3	1472.2	87.4	113306	6	AX646815 Sequence
4	1472.2	87.4	218186	9	AC083865 Homo sapi
5	1462.6	86.9	162268	9	AC146385 Pan trogl
6	1228.6	73.0	1336	6	AX709193 Sequence
7	1106.2	65.7	1340	6	AX709194 Sequence
8	1106.2	65.7	1460	6	AX709195 Sequence
9	1030	61.2	1499	6	AX451925 Sequence
10	991.2	58.9	1051	6	AX453412 Sequence
11	930.4	55.2	1332	6	CQ737895 Sequence
12	916.4	54.4	918	6	BD187510 Novel Pol
13	916.4	54.4	918	6	AX481576 Sequence
14	916.4	54.4	918	6	AX498180 Sequence
15	916.4	54.4	918	6	BD105324 Novel G p
16	916.4	54.4	918	6	AX288420 Homo sapi
17	884.2	52.5	140539	2	AC079758 Homo sapi
18	725.6	43.1	206999	10	AC122886 Mus muscu
19	690	41.0	972	6	AX657538 Sequence

C	20	639.6	38.0	167316	2	AC078995	AC078995 Mus muscu
C	21	634.8	37.7	918	10	AY288427	AY288427 Mus muscu
C	22	605.2	35.9	228766	2	AC099132	AC099132 Rattus no
C	23	456	27.1	456	9	AY255538	AY255538 Homo sapi
C	24	433	25.7	744	10	AY288432	AY288432 Rattus no
C	25	404.4	24.0	447	6	AX147776	AX147776 Sequence
C	26	404.4	24.0	447	6	AX521825	AX521825 Sequence
C	27	275.2	16.3	393	10	AY255553	AY255553 Mus muscu
C	28	184	10.9	169155	5	EX088685	EX088685 Zebrafish
C	29	184	10.9	173882	5	EX640462	EX640462 Zebrafish
C	30	152.2	9.0	162925	2	AC018528	AC018528 Homo sapi
C	31	152.2	9.0	165120	9	AC083860	AC083860 Homo sapi
C	32	144.8	8.6	897	6	BD182016	BD182016 Homo sapi
C	33	131.4	7.8	187649	9	AC146213	AC146213 Pan trogl
C	34	103.4	6.1	140539	2	AC079758	AC079758 Homo sapi
C	35	103.4	6.1	225912	2	AC084210	AC084210 Homo sapi
C	36	76.4	4.5	1113	6	AX280917	AX280917 Sequence
C	37	76.4	4.5	1113	9	AY268428	AY268428 Homo sapi
C	38	76.4	4.5	1113	9	CR542082	CR542082 Homo sapi
C	39	76.4	4.5	1252	9	HUMODRLP	140949 Homo sapien
C	40	76.4	4.5	1379	9	AF348323	AF348323 Homo sapi
C	41	76.4	4.5	1805	6	AX746239	AX746239 Sequence
C	42	76.4	4.5	1973	6	AR270828	AR270828 Sequence
C	43	76.4	4.5	1973	6	AR380872	AR380872 Sequence
C	44	76.4	4.5	1973	9	HSORL1	X77130 H. sapiens m
C	45	76.4	4.5	2534	6	AX548923	AX548923 Sequence

ALIGNMENTS

RESULT 1	AX147836	Sequence 81 from Patent WO0136473.	2525 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX147836					
DEFINITION	AX147836					
ACCESSION	AX147836.1	GI:14346839				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens	(human)				
	Homo sapiens					
REFERENCE						
1	Vogeli, G., Wood, L.S., Parodi, L.A., Hiesch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kayes, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T., and Huff, R.M.					
TITLE	Novel 9 protein-coupled receptors					
JOURNAL	Patent: WO 0136473-A 81 25-MAY-2001;					
PHARMACIA & UPJOHN COMPANY (US)						
FEATURES						
source						
	1. 2525					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
Query Match	87.4%	Score 1472.6;	DB 6;	Length 2525;		
Best Local Similarity	99.6%	Pred. No. 0;				
Matches 1497;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 2;		
QY	153	AAATGACCTTCCCAAGTAAAGCTGCGCAAAATCTCCAGAAATCTCTTGCATCTT	212			
DB	9	ACAGGACCTTCCCAAGTAAAGCTGCGCAAAATCTCCAGAAATCTCTTGCATCTT	68			
QY	213	ATATGACACCCACCTTAATCAGCTCTTCACTAGTGCTTATTTGGCGGGCTGTGGGT	272			
DB	69	ATATGACACCCACCTTAATCAGCTCTTCACTAGTGCTTATTTGGCGGGCTGTGGGT	128			
QY	273	GTCATTTCACTTCTTTCTCTCTGTTGAATGAACCCCGTCACTGACCACTATGGCG	332			
DB	129	GTCATTTCACTTCTTTCTCTCTGTTGAATGAACCCCGTCACTGACCACTATGGCG	188			
QY	333	GTCATTTCACTTGT	392			

Db 189 GTATTAACCTTGGGATGCTCAAGGCTTTTCTGTCAGACAGTCATTTGCTTAC 248
Qy 393 TACTCATCAAGAAAGCTTGGATGTTGGGCTGCCCTTTCGCAATTTTGGAGTGCATG 452
Db 249 TACTCATCAAGAAAGCTTGGATGTTGGGCTGCCCTTTCGCAATTTTGGAGTGCATG 308
Qy 453 CTGACATCAAGATGATCTCAAGTTCCTATTCTATGTTGGGATCCTGGTCAACAGATAC 512
Db 309 CTGACATCAAGATGATCTCAAGTTCCTATTCTATGTTGGGATCCTGGTCAACAGATAC 368
Qy 513 CTGATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAAATGCAATGCTGGCT 572
Db 369 CTGATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAAATGCAATGCTGGCT 428
Qy 573 GCCAGTCTGGCATGTTGAGAGCTGGTATGTCATTTGGTGAACCCCTGGTGTCTCCCG 632
Db 429 GCCAGTCTGGCATGTTGAGAGCTGGTATGTCATTTGGTGAACCCCTGGTGTCTCCCG 488
Qy 633 TATGGAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCACAAAAGCTTGT 692
Db 489 TATGGAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTCACAAAAGCTTGT 548
Qy 693 TACACATATGTAAGAAATCACTAATATGATAGTCAATTTTGTCAATAGCCGTGCTGTG 752
Db 549 TACACATATGTAAGAAATCACTAATATGATAGTCAATTTTGTCAATAGCCGTGCTGTG 608
Qy 753 ATTCTGTTGGTCTTCCAGGCTTCTCATATTAATGTTGTCAGAAAGCTAACCCCATCT 812
Db 609 ATTCTGTTGGTCTTCCAGGCTTCTCATATTAATGTTGTCAGAAAGCTAACCCCATCT 668
Qy 813 TTACTATCCACAGAGATCTGGGCTCAGCTGAAAAACCTAATTTTATAGGGGCTATC 872
Db 669 TTACTATCCACAGAGATCTGGGCTCAGCTGAAAAACCTAATTTTATAGGGGCTATC 728
Qy 873 CTGTGTTGTTCTTCCCTACCAAGTCTTTAGATCTAATTAATGTTGTCAGCGCAT 932
Db 729 CTGTGTTGTTCTTCCCTACCAAGTCTTTAGATCTAATTAATGTTGTCAGCGCAT 788
Qy 933 TCCAAATGCCGTGAGACAAAGTTGATTTTATACAAATCTTCTGATGTATACAGCA 992
Db 789 TCCAAATGCCGTGAGACAAAGTTGATTTTATACAAATCTTCTGATGTATACAGCA 848
Qy 993 ATTAGCTGATGATTTGCTTCTTGTCTTTGGGGGAAGCCATTTGGTTAAGCAAAAG 1052
Db 849 ATTAGCTGATGATTTGCTTCTTGTCTTTGGGGGAAGCCATTTGGTTAAGCAAAAG 908
Qy 1053 ATAAATGGCTTATGGAATGTTGTTTGGCCGTTAGCCACAACTACAGATTCATATTT 1112
Db 909 ATAAATGGCTTATGGAATGTTGTTTGGCCGTTAGCCACAACTACAGATTCATATTT 968
Qy 1113 GCTTCTTTATTTATGGGAAT-AAAAATGGATATAGGGAGGTAAAGATGTTTCAATTAC 1171
Db 969 GCTTCTTTATTTATGGGAATTTAAATAGGTATAGGGAGGTAAAGATGTTTCAATTAC 1028
Qy 1172 TTGATCAAAACATGCTTGTATGTACCAAAACAAAGAGCTATTTAAATGCAAGAGCCCT 1231
Db 1029 TTGATCAAAACATGCTTGTATGTACCAAAACAAAGAGCTATTTAAATGCAAGAGCCCT 1088
Qy 1232 CATTTAGTCTTATGGAATCCCTCCCATCTGTAGTATGCGGTACAAAGACAGTGT 1291
Db 1089 CATTTAGTCTTATGGAATCCCTCCCATCTGTAGTATGCGGTACAAAGACAGTGT 1148
Qy 1292 TGTGTAATCAACCTGAGGTTGCAATATTAATTTTCCAGTACAGAAATGCTGTGTGG 1351
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Qy 1352 CCATGAAGCAACATAGTTTAAAGATTATAGATTTCATTAAGCTCATTAAGTTC 1411
Db 1209 CCATGAAGCAACATAGTTTAAAGATTATAGATTTCATTAAGCTCATTAAGTTC 1267
Qy 1412 CTCTGTTGAAGCAAGTCTCTTAAGTTTGAAGTGAAGTCAAGCTTATAGTTCTTTTCA 1471

Db 1268 CTCTGTTGAAGCATGCTCTTAGGTTTGGACTGAACCTTAGTCTTTTCA 1327
Qy 1472 TCCCATCTTCAACCTTAGTAAATTTTGGCCACACACAGTCCAAAGACAAATC 1531
Db 1328 TCCCATCTTCAACCTTAGTAAATTTTGGCCACACACAGTCCAAAGACAAATC 1387
Qy 1532 TCCCTGCTTAAACAGGTTAGATGCTCCATTTCAATCTCATGCCCCGTATTAAG 1591
Db 1388 TCCCTGCTTAAACAGGTTAGATGCTCCATTTCAATCTCATGCCCCGTATTAAG 1447
Qy 1592 GGAGAAATGATTAATAATTTTCTAGGGATCATTAATCTGTGTAAGAAATCATCTGTCT 1651
Db 1448 GGAGAAATGATTAATAATTTTCTAGGGATCATTAATCTGTGTAAGAAATCATCTGTCT 1507
Qy 1652 AGA 1654
Db 1508 AGA 1510

RESULT 2
AX521885
LOCUS
DEFINITION
Sequence 81 from Patent WO2064789.
AX521885
ACCESSION
AX521885.1 GI:24410791
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
Lind, P., Parodi, L.A., Vogel, G. and Wood, L.S.
TITLE
G protein-coupled receptor
JOURNAL
Patent: WO 02064789-A 81 22-AUG-2002;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
Location/Qualifiers
source
1..2525
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 87.4%; Score 1472.6; DB 6; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 153 AAATGACTTCCCAAGTATGCTGGCCAAATACCTTCAGAAATTCCTTGGCATCCT 212
Db 9 ACAGTGACTTCCCAAGTATGCTGGCCAAATACCTTCAGAAATTCCTTGGCATCCT 68
Qy 213 ATAGTACACCCCACTTAATCAGCCCTCACTCATATGCTTAATGGCGGCTGGGGT 272
Db 69 ATAGTACACCCCACTTAATCAGCCCTCACTCATATGCTTAATGGCGGCTGGGGT 128
Qy 273 GTCAATTCATTTCTTCTCTGCTGTAAGAAATGAACACCCGGTCACTGACCAATGGG 332
Db 129 GTCAATTCATTTCTTCTCTGCTGTAAGAAATGAACACCCGGTCACTGACCAATGGG 188
Qy 333 GTCAATTCATTTGCTGCTGCTCAACAGCGTTTTTCTGCTGACAGTGCATTTGCTTGACC 392
Db 189 GTCAATTCATTTGCTGCTGCTCAACAGCGTTTTTCTGCTGACAGTGCATTTGCTTGACC 248
Qy 393 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGGCCCTTTCGCAAAATTTGAGTGCATG 452
Db 249 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGGCCCTTTCGCAAAATTTGAGTGCATG 308
Qy 453 CTGACATCAACATGATCTCAAGTCTAATTTCTATGTTGGTATCTGTGTCACAGATAC 512
Db 309 CTGACATCAACATGATCTCAAGTCTAATTTCTATGTTGGTATCTGTGTCACAGATAC 368
Qy 513 CTGATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAAATGCAATGCTGTGGCT 572
Db 369 CTGATCTTCTTCAAGTCAAGAAACAAAGTGAATTTCTACAGAAAATGCAATGCTGTGGCT 428


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Db      11884  CATTCTTCAGAGCAAGCAAGCAAGGAAATCTACAGAAAACGTGACTGTGGCTGC 11943
Qy      575    CAGGCTGGAGATGGACGCTGGTGAATGTCATTTGNGATACCCCTGGTGTCTCCGGSTA 634
Db      11944  CAGGCTGGAGATGGACGCTGGTGAATGTCATTTGNGATACCCCTGGTGTCTCCGGSTA 12003
Qy      635    TGGAAATCATGAGAAATACATGAGAGCACTGTTTTAAATTTTCACAAAGAGCTGGCTTA 694
Db      12004  TGGAAATCATGAGAAATACATGAGAGCACTGTTTTAAATTTTCACAAAGAGCTGGCTTA 12063
Qy      695    CACATATGTGAAAATCATCAACTATATGATGTCATTTTGTCAATAGCCGTGTGTGAT 754
Db      12064  CACATATGTGAAAATCATCAACTATATGATGTCATTTTGTCAATAGCCGTGTGTGAT 12123
Qy      755    TCTGTTGGTCTCCAGGCTTCATCATATGATGTCATTTGTCAGAAAGCTAGCCACTCTT 814
Db      12124  TCTGTTGGTCTCCAGGCTTCATCATATGATGTCAGAAAGCTAGCCACTCTT 12183
Qy      815    ACTATCCACACAGAGATCTGGGCTCAGTGAATAAAACCTATTTTATAGGGGTCACTCT 874
Db      12184  ACTATCCACACAGAGATCTGGGCTCAGTGAATAAAACCTATTTTATAGGGGTCACTCT 12243
Qy      875    TGTGTTGTTCTTCCCTTACCAAGTCTTTAGAGATCTATTAAGTGTGACGCAATTC 934
Db      12244  TGTGTTGTTCTTCCCTTACCAAGTCTTTAGAGATCTATTAAGTGTGACGCAATTC 12303
Qy      935    CAATGCTGTAGACGCAAGGTCATTTTAAAGAAATCTCTGTGAGTCATAAGCAAT 994
Db      12304  CAATGCTGTAGACGCAAGGTCATTTTAAAGAAATCTCTGTGAGTCATAAGCAAT 12363
Qy      995    TAGCTGTATGATTTGCTCTCTTGTCTTTGGGGAGAGCAATGTTTAAAGCAAAAGAT 1054
Db      12364  TAGCTGTATGATTTGCTCTCTTGTCTTTGGGGAGAGCAATGTTTAAAGCAAAAGAT 12423
Qy      1055  AATTGGCTTATGGAATTTGTTTGGCCGTAGCCCAAACTACAGTATTCATATTGTC 1114
Db      12424  AATTGGCTTATGGAATTTGTTTGGCCGTAGCCCAAACTACAGTATTCATATTGTC 12483
Qy      1115  TTCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGAGTAAGATGTTTATTAATTA 1173
Db      12484  TTCTTTATATTTGGGAATTTAAATGGGTATAGGGAGAGTAAGATGTTTATTAATTA 12543
Qy      1174  GATCAAAAACCATGCTTGATGTATCCCAAAACAAAGAGACTATAAATGCAAGAGCCCTCA 1233
Db      12544  GATCAAAAACCATGCTTGATGTATCCCAAAACAAAGAGACTATAAATGCAAGAGCCCTCA 12603
Qy      1234  TTGTAATCTTTATGGGATCCCTCCATCTGAGTGTGCGCGTAACAAAGACAGTGTG 1293
Db      12604  TTGTAATCTTTATGGGATCCCTCCATCTGAGTGTGCGCGTAACAAAGACAGTGTG 12663
Qy      1294  TTGAATCCACTGGAGTTGCAATTTATCATTTTCCAGTACAGAAATGTCGTGGGCC 1353
Db      12664  TTGAATCCACTGGAGTTGCAATTTATCATTTTCCAGTACAGAAATGTCGTGGGCC 12723
Qy      1354  CATGAAAGCAACATAGGTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTCT 1413
Db      12724  CATGAAAGCAACATAGGTTTAAAGATTTT-AGAGTTTCAATTAAGTCTCATTAAGTTCT 12782
Qy      1414  CTGTTTGAAGATGTCCTTTAGGTTTGGATGTAATCTGAGACTGAGACTTTTATGTTTCAT 1473
Db      12783  CTGTTTGAAGATGTCCTTTAGGTTTGGATGTAATCTGAGACTGAGACTTTTATGTTTCAT 12842
Qy      1474  CCACTTCAACATAGGTAATTTCTGGACACACACCACTCCAAAGACACAAACCTCTC 1533
Db      12843  CCACTTCAACATAGGTAATTTCTGGACACACACCACTCCAAAGACACAAACCTCTC 12902
Qy      1534  CTTGCTTACCAAGTTAGATGTCCTCATTCATCTCATGCTCTGATTTAAATCTGATTA 1593
Db      12903  CTTGCTTACCAAGTTAGATGTCCTCATTCATCTCATGCTCTGATTTAAATCTGATTA 12962
Qy      1594  AGGAAATGTTAAATTTTCTAGGATTCATTAATCTGTTAGGAAATCATCTGTCTAG 1653

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Db      12963  AGAATATGTTAAATTTTCTAGGGTATCATTAATCTGTAGAGAAATCATCTGTCTAG 13022
Qy      1654  A 1654
Db      13023  A 13023

RESULT 4
AC083865      218186 bp      DNA      linear      PRI 26-JAN-2001
LOCUS      AC083865
DEFINITION      Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION      AC083865
VERSION      AC083865.2  GI:12545315
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Large-scale Mapping and Sequencing of Human Chromosome 7
2 (bases 1 to 218186)
Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
Direct Submision
Submitted (04-OCT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Direct Submision
Submitted (26-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
----- Project Information
Center project name: Hsachr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217693 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-ffp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-ffp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': mapping in progress
3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

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This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30) ; an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt
-----------	--------	-----------	--------	-----------	--------

8696	8979	764	755	3414	3439
6	<800	6382	6611	2067	2102
663	<800	512	<800	5356	5585
122	<800	449	<800	1416	1421
174	<800	1059	1063	610	<800
4551	4612	70	<800	225	<800
952	988	424	<800	932	961
968	988	2594	2670	1982	2102
980	988	3852	3908	29	<800
10043	10231	915	918	2663	2719
2412	2471	5333	5315	5958	5921
3670	3625	4795	4869	448	<800
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27	<800	552	<800	1869	1948
9749	10231	1010	1063	3655	3640
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1957	2017	2280	2278	3924	3962
2403	2471	4595	4869	591	<800
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359	<800	2624	2670	572	<800
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2839	2805	11280	11329	614	<800
2787	2805	840	918	7901	8084
5407	5309	9244	8985	619	<800

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7246	7468	3195	3163	345	<800
4508	4455	4273	4301	324	<800
5815	5866	1980	2031	1496	1421
5380	5309	520	<800	6710	6637
339	<800	737	755	71	<800
4809	4612	1833	1878	848	877
571	<800	8798	8985	6153	6135
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956	988	4946	4869	14	<800
2026	2123	6247	6163	44	<800
1821	1788	685	<800	10402	10380
2453	2471	1367	1406	300	<800
8955	9499	109	<800	5150	5294
1004	988	3608	3535	3195	3246
7399	7468	7728	7736	2281	2309
7516	7468	4264	4301	2740	2804
4119	4107	357	<800	5869	5921
193	<800	3645	3709	248	<800
2792	2805	1961	2031	3072	3079
7034	7468	5668	5588	585	<800
4840	4902	957	918	655	<800
603	<800	5024	4869	1206	1270
761	<800	201	<800	1723	1693
2518	2471	1119	1195	19721	20141
4086	4107	709	<800	2331	2309
5916	5835	4907	4869	1940	1993
6995	6947	1161	1195	5574	5585
4667	4612	11292	11329	3867	3865
10434	10231	6699	6611	1268	1270
1306	1313	1358	1406	8347	8084
374	<800	2400	2394	3636	3640

Query Match 87.4%; Score 1472.2; DB 9; Length 218186;

Best Local Similarity 99.7%; Pred. No. 0; Mismatches 3; Indels 2; Gaps 2;

Matches 1496; Conservative 0;

QY 155 ATGTGACTTCCCAAGTATGCTGGCCACATATCTTCAGGAATTCCTTGCGATCTAT 214
DB 133107 AGGTGACTTCCCAAGTATGCTGGCCACATATCTTCAGGAATTCCTTGCGATCTAT 133166
QY 215 AGTGAACCCCACTTATATGCTTACTTATGCTTATTTGGCGGCTGTGGGTGT 274

Db	133167	AGTGAACACCCCACTTATATAGCGCTCTACTTCAATAGTGTATTATGGGGGCGCTGGTGGGTGT	133226
OY	275	CATTTCATTCTTTTCTCTCTGGTGAATAAGAACACCCGGTCAGTGACCAACATGGCGGT	334
Db	133227	CATTTCATTCTTTTCTCTCTGGTGAATAAGAACACCCGGTCAGTGACCAACATGGCGGT	133286
OY	335	CATTAACTGGTGGTGGTCCACAGCGTTTTTTCGCTGACAGTGCATTTTCGCTTGACCTA	394
Db	133287	CATTAACTGGTGGTGGTCCACAGCGTTTTTTCGCTGACAGTGCATTTTCGCTTGACCTA	133346
OY	395	CCTCATCAAGAAGACTTGGATGTGGGAGCGCTTCTGCAAAATTTGTGAGTGCATGCT	454
Db	133447	CCTCATCAAGAAGACTTGGATGTGGGAGCGCTTCTGCAAAATTTGTGAGTGCATGCT	133406
OY	455	GCACATCCACAGTACCTGACGTTTCCCTATTCATGTGGTATCCCTGGTCAACGATACCT	514
Db	133407	GCACATCCACAGTACCTGACGTTTCCCTATTCATGTGGTATCCCTGGTCAACGATACCT	133466
OY	515	CATCTTCTTCAAGTCAAGCAAGACAAAGTGGAAATTTCAACAAAACCTGATGCTGTGC	574
Db	133467	CATCTTCTTCAAGTCAAGCAAGACAAAGTGGAAATTTCAACAAAACCTGATGCTGTGC	133526
OY	575	CAGTCTGGACATGTGACCGCTGGTATTTGTCATGTGGTATCCCTGGTGTCTCCCGTA	634
Db	133527	CAGTCTGGACATGTGACCGCTGGTATTTGTCATGTGGTATCCCTGGTGTCTCCCGTA	133586
OY	635	TGCAATCCATGAGGAATCAATAGAGAGACGTTTTTAATTTCACAAGAGCTTGCTTA	694
Db	133587	TGCAATCCATGAGGAATCAATAGAGAGACGTTTTTAATTTCACAAGAGCTTGCTTA	133646
OY	695	CACATATGTGAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTGCTGTGAT	754
Db	133647	CACATATGTGAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTGCTGTGAT	133706
OY	755	TCTGTGGCTTCCAGAGTCTTCATCATATATGTTGATGGTGGACAGACCTACGCACTTT	814
Db	133707	TCTGTGGCTTCCAGAGTCTTCATCATATATGTTGATGGTGGACAGACCTACGCACTTT	133766
OY	815	ACTATCCCAACAGAGATTCGAGGCTCAGCTGAAAACTATTTTTTATAGGGGTCACTCT	874
Db	133767	ACTATCCCAACAGAGATTCGAGGCTCAGCTGAAAACTATTTTTTATAGGGGTCACTCT	133826
OY	875	TGTTTGTTCCTTCCCTACCACTTCTTTAGATCTATTACTTGAAATGTTGTGACGATTC	934
Db	133827	TGTTTGTTCCTTCCCTACCACTTCTTTAGATCTATTACTTGAAATGTTGTGACGATTC	133886
OY	935	CAATGCCGTGACAGCAAGGTGCAATTTTATATACGAAATCTTCTTGAAGTAAACAGCAAT	994
Db	133887	CAATGCCGTGACAGCAAGGTGCAATTTTATATACGAAATCTTCTTGAAGTAAACAGCAAT	133946
OY	995	TAGCTGTATGATTTGCTTCTTGTCTTTGGGGAGCCATGTGTTTAAACAAAAGAT	1054
Db	133947	TAGCTGTATGATTTGCTTCTTGTCTTTGGGGAGCCATGTGTTTAAACAAAAGAT	134006
OY	1055	AATGGCTTATGGAATGTGTTTGTGGCGTTAAGCCAAACATCAAGTATTCATATTCG	1114
Db	134007	AATGGCTTATGGAATGTGTTTGTGGCGTTAAGCCAAACATCAAGTATTCATATTCG	134066
OY	1115	TTCTTTTATATTTGGGAAT-AAAATGGATATAGGGAGGTAAAGATGGTATTTTCATTACT	1173
Db	134067	TTCTTTTATATTTGGGAAT-AAAATGGATATAGGGAGGTAAAGATGGTATTTTCATTACT	134126
OY	1174	GATCAAAACCAAGCTTGATGTATACCAAAACAAAGAGACTTATTAATGCAAGAGCCCTCA	1233
Db	134127	GATCAAAACCAAGCTTGATGTATACCAAAACAAAGAGACTTATTAATGCAAGAGCCCTCA	134186
OY	1234	TTGTATGCTTATATGGGAATCCCTCCATCTCTAGATGATGGCGTACAAAGACCAAGTGTG	1293
Db	134187	TTGTATGCTTATATGGGAATCCCTCCATCTCTAGATGATGGCGTACAAAGACCAAGTGTG	134246
OY	1294	TTGAATCCAAGTGGATGCAATATTTACATTAATTTTCAGATACAGATGTCTGTGTGCC	1353

Db	13424	PTBAAITCAACCTGGAGTTGCACATATTACATTAATTTTCCAGTAGACGAANNGTCGTGTCGCC	134306
Oy	1354	CATGAAGAACAATAGCTTTTAAAGCTTTTAAAGCTTCATTAGCTATCTTAAGTTCCCT	1413
Db	134307	CATGAAGAACAATAGCTTTTAAAGCTTTT-AAAGCTTCATTAGCTATCTTAAGTTCCCT	134365
Oy	1414	CTGTTTGAAGCAACGGCTCTTAGCTTTTGAACCTGACCTTTAGTTCTTTTCATC	1473
Db	134366	CTGTTTGAAGCAATGGCTCTTAGCTTTTGAACCTGACCTTTAGTTCTTTTCATC	134425
Oy	1474	CCACTTCACCATPAGTGAAGTAATAATTCGTGCCACACCCAGCTCCAAAGACAAACTCTC	1533
Db	134426	CCACTTCACCTTAGGTAAGTAATAATTCGTGCCACACCCAGCTCCAAAGACAAACTCTC	134485
Oy	1534	CTTCGCTAACCCAGTTAGTAGTGTCCCATTCATCTCATGCGCTGATTAATAAATGATAAGGG	1593
Db	134486	CTTCGCTAACCCAGTTAGTAGTGTCCCATTCATCTCATGCGCTGATTAATAAATGATAAGGG	134545
Oy	1594	AGAGAATAGTTAAATAATTTTCTAGGATCATTAACCTGTGTAAGAAGTCATCTGTCTAG	1653
Db	134546	AGAGAATAGTTAAATAATTTTCTAGGATCATTAACCTGTGTAAGAAGTCATCTGTCTAG	134605
Oy	1654	A 1654	
Db	134606	A 134606	
RESULT 5	AC146385		
LOCUS	AC146385	162268 bp	DNA linear PRI 19-MAY-2004
DEFINITION	Pan troglodytes BAC clone RP43-126C6 from 7, complete sequence.		
ACCESSION	AC146385		
VERSION	AC146385.4	GI:46391241	
KEYWORDS	HTG.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
AUTHORS	Krucowski,S., Bielik,L. and Haglund,K.		
JOURNAL	The sequence of Pan troglodytes BAC clone RP43-126C6		
REFERENCE	Unpublished (2001)		
AUTHORS	2 (bases 1 to 162268)		
JOURNAL	Wilson,R.K.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444		
JOURNAL	Forest Park Parkway, St. Louis, MO 63108, USA		
REFERENCE	3 (bases 1 to 162268)		
AUTHORS	Wilson,R.K.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (15-APR-2004) Genetics, Genome Sequencing Center, 4444		
AUTHORS	Forest Park Parkway, St. Louis, MO 63108, USA		
JOURNAL	5 (bases 1 to 162268)		
REFERENCE	Wilson,R.K.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (19-MAY-2004) Washington University School of Medicine,		
REFERENCE	Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO		
AUTHORS	63108, USA		
JOURNAL	On Apr 15, 2004 this sequence version replaced gi:42734595.		
COMMENT	----- Genome Center		
	Center: Washington University Genome Sequencing Center		
	Center code: WUGSC		
	Web site: http://genome.wustl.edu		
	Contact: submissions@wustl.edu		
	----- Summary Statistics		
	Center project name: C_P126C06		

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:

The RPECI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Cline', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from Resgen
(<http://www.resgen.com>) or Pieter de Jong and co-workers at
<http://www.bacpac.chori.org>.

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is
overlapped by AC146047

Location/Qualifiers

Source
1. 162268
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/map="7"
/clone="RP43-126C6"
/clone_1lb="RPECI-43"
138009. 138038
/note="Sequence derived from one plasmid subclone."

ORIGIN

unseqre

Query Match 86.9%; Score 1462.6; DB 9; Length 162268;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1490; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 155 ATGTGACTTCCCAAGTATGCTGGCCACAAATACCTCCAGAAATCTCTTGGATCTCTAT 214
DB 146132 AGGTGACTTCCCAAGTATGCTGGCCACAAATACCTCCAGAAATCTCTTGGATCTCTAT 146191
QY 215 AGTACACCCCACTTAATCAGCCTCTACTATGATGCTTATTTGGCGGCGTGGGGGT 274
DB 146192 AGTACACCCCACTTAATCAGCCTCTACTATGATGCTTATTTGGCGGCGTGGGGGT 146251
QY 275 CATTTCCATCTTTTCTCTCTGTAATAATGACACCCGCTCAGTGAACCAATGCGGT 334
DB 146252 CATTTCCATCTTTTCTCTCTGTAATAATGACACCCGCTCAGTGAACCAATGCGGT 146311
QY 335 CATTAACCTGGTGGTGCACAGCGTTTTCTGCTGACAGTGCACATTCGCTTGACCTA 394
DB 146312 CATTAACCTGGTGGTGCACAGCGTTTTCTGCTGACAGTGCACATTCGCTTGACCTA 146371
QY 395 CCTCATCAAGAAAGCTTGGATGTTGGGCTGCCCTTGCAGAAATTTTGGAGTGGCAAGCT 454
DB 146372 CCTCATCAAGAAAGCTTGGATGTTGGGCTGCCCTTGCAGAAATTTTGGAGTGGCAAGCT 146431
QY 455 GCACATCAAGTATGCTCAGTTCCTATTCTATGTTGGTGAATCCGTGCACAGATACCT 514
DB 146432 GCACATCAAGTATGCTCAGTTCCTATTCTATGTTGGTGAATCCGTGCACAGATACCT 146491
QY 515 CATCTTCTTCAAGTGCAAGCAAGAGTGAATTTCTACAGAAATCTGACGTGTGGCTGC 574
DB 146492 CATCTTCTTCAAGTGCAAGCAAGAGTGAATTTCTACAGAAATCTGACGTGTGGCTGC 146551
QY 575 CAGTGCTGCAATGTGAGCGCTGGTATTTGTCATTTGTGTGTAACCTGGTGTCTCCGGTA 634

DB 146552 CAGTGCTGCAATGTGAGCGCTGGTATTTGTCATTTGTGTGTAACCTGGTGTCTCCGGTA 146611
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DB 146612 TGAATCAATGAGGAATPAACAATGAGAGCACTGTTTAAATTTCAACAAGAGCTTGCTTA 146671
QY 695 CAGTAATGTAAATTCATCAACTATATGATATGATATTTTGTCTAACCCTGGTGGTAT 754
DB 146672 CAGTAATGTAAATTCATCAACTATATGATATGATATTTTGTCTAACCCTGGTGGTAT 146731
QY 755 TCTGTTGATCTCCAGGCTTTCATCATTTATGATGATGTCAGAGGACGACCTCTT 814
DB 146732 TCTGTTGATCTCCAGGCTTTCATCATTTATGATGATGTCAGAGGACGACCTCTT 146791
QY 815 ACTATCCACAGAGATTTGGGCTCAGCTGAGTAAACCTATTTTATAGGGTATCT 874
DB 146792 ACTATCCACAGAGATTTGGGCTCAGCTGAGTAAACCTATTTTATAGGGTATCT 146851
QY 875 TGTGTTGTTCTTCCCTACAGATTTTATAGATCTATTTACTTGAATGTTGAGAGCTTC 934
DB 146852 TGTGTTGTTCTTCCCTACAGATTTTATAGATCTATTTACTTGAATGTTGAGAGCTTC 146911
QY 935 CAATGCCCTGAGCAGAAAGTGCATTTTATTAACGAATCTTCTTGAAGTGAACGAAT 994
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QY 995 TAGCTGCTATGATTTGCTCTCTTGTCTTGGGGAGGACATTTGTTAAGCAAAAGAT 1054
DB 146972 TAGCTGCTATGATTTGCTCTCTTGTCTTGGGGAGGACATTTGTTAAGCAAAAGAT 147031
QY 1055 AATTGGCTTATGAAATGTTGTTTGGCGGTAGCCCAAACTACATATTTCTATTTGC 1114
DB 147032 AATTGGCTTATGAAATGTTGTTTGGCGGTAGCCCAAACTACATATTTCTATTTGC 147091
QY 1115 TTCCTTATATTTGGGAAT-AAAATGGGTATAGGGAGAGTAAAGTGTATTTCTACTT 1173
DB 147092 TTCCTTATATTTGGGAAT-AAAATGGGTATAGGGAGAGTAAAGTGTATTTCTACTT 147151
QY 1174 GATCAAAACATGCTTGTATGATACCAAAACAAAGACATTAATAATGCAAGGCCCTCA 1233
DB 147152 GATCAAAACATGCTTGTATGATACCAAAACAAAGACATTAATAATGCAAGGCCCTCA 147211
QY 1234 TTGTATGCTTATGAGATCCCTCCATCTCTGAGTATGCGCGTACAAAGACAGTGTG 1293
DB 147212 TTGTATGCTTATGAGATCCCTCCATCTCTGAGTATGCGCGTACAAAGACAGTGTG 147271
QY 1294 TTGAATCACCTGAGTGAATTAATTAATTTTTCAGTACAGAAATGTCGTGGTGGC 1353
DB 147272 TTGAATCACCTGAGTGAATTAATTAATTTTTCAGTACAGAAATGTCGTGGTGGC 147331
QY 1354 CATGAAGCAACATAGGTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTT 1413
DB 147332 CATGAAGCAACATAGGTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTT 147390
QY 1414 CTGTTTGAAGCATGCTCTTTAGGTTTGAATGAACTCAAGACCTTTAGTTCTTTTCATC 1473
DB 147391 CTGTTTGAAGCATGCTCTTTAGGTTTGAATGAACTCAAGACCTTTAGTTCTTTTCATC 147450
QY 1474 CCACTTCAACATAGTGAATTAATTCGAGCACACCACTCCCAAGACAAACCTCTC 1533
DB 147451 CCACTTCAACATAGTGAATTAATTCGAGCACACCACTCCCAAGACAAACCTCTC 147510
QY 1534 CTTCGCTAACAGGTTATGATGCTCCATTCATCTCACTGCTCTGATTAATAAAGAGG 1593
DB 147511 CTTCGCTAACAGGTTATGATGCTCCATTCATCTCACTGCTCTGATTAATAAAGAGG 147570
QY 1594 AGAAGATATGTTAAATTTTCTTAAAGGATCATTAACCTGTTGAGAAATCATCTGTCTAG 1653
DB 147571 AGAAGATATGTTAAATTTTCTTAAAGGATCATTAACCTGTTGAGAAATCATCTGTCTAG 147630
QY 1654 A 1654

Db 147631 A 147631

RESULT 6
AX709193 1336 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 52 from Patent WO02063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
1 G-protein coupled receptors
Patent: WO 02063004-A 52.15-AUG-2002;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1.1336
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012430CB1"

ORIGIN
Query Match 73.0%; Score 1228.6; DB 6; Length 1336;
Best Local Similarity 99.6%; Pred. No. 2.7e-307;
Matches 1242; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 29 TCTTCTAGCAATGATTTTCAACATTTATTAATGAAGTTGTAGACTGATTAAGAGATGC 88
DB 77 TTTTCAGCAATGATTTTCAACATTTATTAATGAAGTTGTAGACTGATTAAGAGATGC 136
QY 89 TCAGCTAAGGAGATTCCTGATGAGCTTTTATGATTAATCAATCCTCTGAAATTCAT 148
DB 137 TCAGCTAAGGAGATTCCTGATGAGCTTTTATGATTAATCAATCCTCTGAAATTCAT 196
QY 149 GCAAAATGTACTTCCCAAGTATGCTGAGCAATATCCCGAGAATTCCTTSCGA 208
DB 197 GCAAAATGTACTTCCCAAGTATGCTGAGCAATATCCCGAGAATTCCTTSCGA 256
QY 209 TCTATAGTACACCCCACTTAATCAGCTTCTATCATAGTGTATTTGGCGGCTGT 268
DB 257 TCTATAGTACACCCCACTTAATCAGCTTCTATCATAGTGTATTTGGCGGCTGT 316
QY 269 GGGGTGATTTCCATTTCTTTTCCCTGCTGTAATAAACAACCCGGTCAATGACACAT 328
DB 317 GGGGTGATTTCCATTTCTTTTCCCTGCTGTAATAAACAACCCGGTCAATGACACAT 376
QY 329 GGGGTGATTTCCATTTCTTTTCCCTGCTGTAATAAACAACCCGGTCAATGACACAT 388
DB 377 GGGGTGATTTCCATTTCTTTTCCCTGCTGTAATAAACAACCCGGTCAATGACACAT 436
QY 389 GACCTACCTCATCAAGAAGCTTGATGTTGGCTCCCTTCTGCAAAATTTTGATGTC 448
DB 437 GACCTACCTCATCAAGAAGCTTGATGTTGGCTCCCTTCTGCAAAATTTTGATGTC 496
QY 449 CATCTGACATCAATGATGATGCTGATGTTCTATGATGATGATCTGCTGATGATG 508
DB 497 CATCTGACATCAATGATGATGCTGATGTTCTATGATGATGATCTGCTGATGATG 556
QY 509 ATACCTCATCTTTCTTCAAGTCAAGAAGCAAGTGAATTCACAGAATACTGATGCT 568
DB 557 ATACCTCATCTTTCTTCAAGTCAAGAAGCAAGTGAATTCACAGAATACTGATGCT 616
QY 569 GGCTGCAAGTCTGGCATGTGAGCGCTGTGATGTCATGTGTGATACCCCTGTGTCTC 628

Db 617 GGCTGCAAGTCTGGCATGTGAGCGCTGTGATGTCATGTGTGATACCCCTGTGTCTC 676
QY 629 CCGGTATGAAATCCATGAGAAATACATAGAGACATCTTTTAAATTTCAAAAAGCT 688
DB 677 CCGGTATGAAATCCATGAGAAATACATAGAGACATCTTTTAAATTTCAAAAAGCT 736
QY 689 TGCTTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
DB 737 TGCTTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 796
QY 749 TGTGATCTGTGTGTCTTCCAGGCTTCAATATGATGATGATGATGATGATGATG 808
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QY 809 CTCCTTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
DB 857 CTCCTTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 916
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DB 917 CATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 976
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DB 977 GCATTCATATGCTGTGAGACAGAGGTCATTTATTAACGAATCTTGTGATGATG 1036
QY 989 AGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1048
DB 1037 AGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
QY 1049 AAGATATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1108
DB 1097 AAGATATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1156
QY 1109 ATTGCTTCTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
DB 1157 ATTGCTTCTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1216
QY 1168 TTACTGATCAAAACCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1227
DB 1217 TTACTGATCAAAACCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1276
QY 1228 CCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1274
DB 1277 CCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323

RESULT 7
AX709194 1340 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 53 from Patent WO02063004.
ACCESSION AX709194
VERSION AX709194.1 GI:29564788
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
1 G-protein coupled receptors
Patent: WO 02063004-A 53.15-AUG-2002;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1.1340
/organism="Homo sapiens"
/mol_type="unassigned DNA"

/db_xref="taxon:9606"
/note="Incyte ID No: 90012586CB1"

ORIGIN

Query Match 65.7%; Score 1106.2; DB 6; Length 1340;
Best Local Similarity 99.6%; Pred. No. 1.5e-275;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

153 AATGAGCTTCCCAAGATGCTGCGCCACAAATCCTCCAGAAATTCCTCTGGGATCT 212
205 ACAGGTGACTTCCCAAGATGCTGCGCCACAAATCCTCCAGAAATTCCTCTGGGATCT 264
213 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTAATGGCGGGCTGGTGGT 272
265 ATAGTGACACCCCACTTAATCAGCTCTACTTCACTATGCTTAATGGCGGGCTGGTGGT 324
273 GTCATTTCCATTTCTTTCTCTCTGCTGTAAGAAATGAAACCCGGTCAAGACCAATGGCG 332
325 GTCATTTCCATTTCTTTCTCTCTGCTGTAAGAAATGAAACCCGGTCAAGACCAATGGCG 384
333 GTCATTAATCTTGT 392
385 GTCATTAATCTTGT 444
393 TACCTCATCAAGAAAGATTTGGATTTGGGCTGCGCTTTCGCAAAATTTGGAGTGCATG 452
445 TACCTCATCAAGAAAGATTTGGATTTGGGCTGCGCTTTCGCAAAATTTGGAGTGCATG 504
453 CTGCAATCCACATGTATCTCAAGCTTCTTCTATGATGATGATGATGATGATGATGATGATG 512
505 CTGCAATCCACATGTATCTCAAGCTTCTTCTATGATGATGATGATGATGATGATGATGATG 564
513 CTGATCTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCT 572
565 CTGATCTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCT 624
573 GCCAGTCTGGCATGT 632
625 GCCAGTCTGGCATGT 684
633 TATGGAATCCATGAGAAATCAATGAGAGACAGTCTTAAATTTTCAAAAGAGCTGTCT 692
685 TATGGAATCCATGAGAAATCAATGAGAGACAGTCTTAAATTTTCAAAAGAGCTGTCT 744
693 TACACATATGTGAATAATCATCACTATATGATGATGATGATGATGATGATGATGATGATG 752
745 TACACATATGTGAATAATCATCACTATATGATGATGATGATGATGATGATGATGATGATG 804
753 ATTCTGTGTGTCTTCCAGGCTTCTCATATATGATGATGATGATGATGATGATGATGATGATG 812
805 ATTCTGTGTGTCTTCCAGGCTTCTCATATATGATGATGATGATGATGATGATGATGATGATG 864
813 TTAATATCCACAGAGAGTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGCTGATC 872
865 TTAATATCCACAGAGAGTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGCTGATC 924
873 CTGTGTGTGTCTTCCCTCAAGTCTTGAATCTATATGATGATGATGATGATGATGATGATGATG 932
925 CTGTGTGTGTCTTCCCTCAAGTCTTGAATCTATATGATGATGATGATGATGATGATGATGATG 984
933 TCCAAATGCTGTAGACAGAAAGTGTGATTTTATAGAAATCTTCTGAGTGTAGACGA 992
985 TCCAAATGCTGTAGACAGAAAGTGTGATTTTATAGAAATCTTCTGAGTGTAGACGA 1044
993 ATTAGCTGTATGATTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
1045 ATTAGCTGTATGATTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1104
1053 ATTAATGGCTTATGAAATGT 1112
1105 ATTAATGGCTTATGAAATGT 1164
1113 GCTTCTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGATGTATTTCAATTAC 1171

Db 1165 GCTTCTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGATGTATTTCAATTAC 1224
1172 TTGATCAAAACCATGCTTGTATGATACCAAAACAAAGAGCTATTAATATCAAGAGCCT 1231
1225 TTGATCAAAACCATGCTTGTATGATACCAAAACAAAGAGCTATTAATATCAAGAGCCT 1284

1232 CATTGTAGTCTTATGAGATCCCTCCCATCTCTGAGTATGCG 1274
1285 CATTGTAGTCTTATGAGATCCCTCCCATCTCTGAGTATGAGC 1327

RESULT 8
AX709195 1460 bp DNA linear PAT 04-APR-2003
Sequence 54 from Patent WO20063004.
AX709195
AX709195.1 GI:29564789
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Baughn, M.R., Tiboule, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Walla, N.K., Ariz, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pel, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Grail, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
G-protein coupled receptors
Patent: WO 02063004-A 54 15-AUG-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 1460
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012670CB1"

FEATURES
source

ORIGIN

Query Match 65.7%; Score 1106.2; DB 6; Length 1460;
Best Local Similarity 99.6%; Pred. No. 1.5e-275;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

153 AATGAGCTTCCCAAGATGCTGCGCCACAAATCCTCCAGAAATTCCTCTGGGATCT 212
325 ACAGGTGACTTCCCAAGATGCTGCGCCACAAATCCTCCAGAAATTCCTCTGGGATCT 384
213 AATGAGACCCCACTTAATCAGCTCTTCAATAGTGTATTTGGCGGGCTGTGGGT 272
385 ATAGTGACACCCCACTTAATCAGCTCTTCAATAGTGTATTTGGCGGGCTGTGGGT 444
273 GTCATTAATCTTGT 332
445 GTCATTAATCTTGT 504
333 GTCATTAATCTTGT 392
505 GTCATTAATCTTGT 564
393 TACCTCATCAAGAAAGATTTGGATTTGGGCTGCGCTTTCGCAAAATTTGGAGTGCATG 452
565 TACCTCATCAAGAAAGATTTGGATTTGGGCTGCGCTTTCGCAAAATTTGGAGTGCATG 624
453 CTGCAATCCACATGTATCTCAAGCTTCTTCTATGATGATGATGATGATGATGATGATGATGATG 512
625 CTGCAATCCACATGTATCTCAAGCTTCTTCTATGATGATGATGATGATGATGATGATGATGATG 684
513 CTGATCTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCT 572
685 CTGATCTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCT 744

QY	5/73	GCACATGCGGCAATGTGACCGCTGGTGATTTGTCATTTGGTGATACCCCGTGTGTCTCCCGG	632
Db	745	GCACATGCTGGCAATGTGACCGCTGGTGATTTGTCATTTGGTGATACCCCGTGTGTCTCCCGG	804
QY	633	TATGAAATCCAAATGAGAAATACAAATAGAGACACTGTTTTTAAATTTCACAAAGAGCTTGCT	692
Db	805	TATGAAATCCAAATGAGAAATACAAATAGAGACACTGTTTTTAAATTTCACAAAGAGCTTGCT	864
QY	633	TACACAAATGTGAAAAATCACTAAATAGATAGTCAATTTTTGTCTAAGCCGTTCTGTG	752
Db	865	TACACAAATGTGAAAAATCACTAAATAGATAGTCAATTTTTGTCTAAGCCGTTCTGTG	924
QY	753	ATTCTGTTGCTTCTCCAGTCTTCACTCAATTAATTTGATGGTGCAAACTTAAGCCCACTCT	812
Db	925	ATTCTGTTGCTTCTCCAGTCTTCACTCAATTAATTTGATGGTGCAAACTTAAGCCCACTCT	984
QY	813	TTACTATCCCAACAGAGATTTCTGGGCTCAGCTGAATAAACTAATTTTTATAGGGGCTCATC	872
Db	985	TTACTATCCCAACAGAGATTTCTGGGCTCAGCTGAATAAACTAATTTTTATAGGGGCTCATC	1044
QY	873	CTTGTGTTGTTCTCTTCCCTTACCAAGTCTTTAGAGATCTAATTACTTGAATGTTGTGACGCA	932
Db	1045	CTTGTGTTGTTCTCTTCCCTTACCAAGTCTTTAGAGATCTAATTACTTGAATGTTGTGACGCA	1104
QY	933	TCCAAATGCGCTTGAAGAGAGAGAGTTCATTTTATACGAAATCTTCTTAAGTGTAACAGCA	992
Db	1105	TCCAAATGCGCTTGAAGAGAGAGTTCATTTTATACGAAATCTTCTTAAGTGTAACAGCA	1164
QY	993	ATTAGCTCTATAGATTTTCTCTCTTTGTCTTTTGGGGGAGAGCAATTGGTTTAAAGCAAA	1052
Db	1165	ATTAGCTCTATAGATTTTCTCTCTTTGTCTTTTGGGGGAGAGCAATTGGTTTAAAGCAAA	1224
QY	1053	ATTAATTTGCTTATAGGAATTTGTTTGTGTCGGTTAGCCACAACACTACAGTATTCATATTT	1112
Db	1225	ATTAATTTGCTTATAGGAATTTGTTTGTGTCGGTTAGCCACAACACTACAGTATTCATATTT	1284
QY	1113	GCTTCCTTTATATATTTGGGAAT-AAAAATGGGTATAGGGGAGGTATAGATGTATTTCAATAC	1171
Db	1285	GCTTCCTTTATATATTTGGGAAT-AAAAATGGGTATAGGGGAGGTATAGATGTATTTCAATAC	1344
QY	1172	TTGATTCAAAACCATGCTCTTGATGTATGCCCAAAACAAAAGAGACTATTAATATGCAAGAGCC	1231
Db	1345	TTGATTCAAAACCATGCTCTTGATGTATGCCCAAAACAAAAGAGACTATTAATATGCAAGAGCC	1404
QY	1232	CATTGTAGTCTTATATGGGATCCCTCCCATCTCTGATGATGAGC 1274	
Db	1405	CATTGTAGTCTTATATGGGATCCCTCCCATCTCTGATGATGAGC 1447	
RESULT 9			
AX451925			
LOCUS	AX451925	1499 bp	DNA
DEFINITION	Sequence 22 from Patent WO0226825.		linear
ACCESSION	AX451925		
KEYWORDS	AX451925.1 GI:21698748		
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1		
	Baughn, M. R., Graul, R. C., Walla, N. K., Gandhi, A. R., Hafalia, A. J.,		
	Raunkumar, J., Tribouley, C. M., Thornton, M., Kallick, D. A., Yao, M. G.,		
	Elliot, V. S., Burford, N., Khan, F. A., Yue, H., Lu, Y., Arvizu, C.,		
	Roopa, R., Nguyen, D. B., Lee, E. A., Lu, D. A., Ison, C. H., Walsh, R. T. and		
	Policky, J. L.		
TITLE	G-protein coupled receptors		
JOURNAL	Patent: WO 0226825-A 22 04-APR-2002;		
FEATURES	Incyte Genomics, Inc. (US)		
	Location/Qualifiers		
SOURCE	1. 1499		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		

	ORIGIN	/db_xref="taxon:9606" /note="Incyte ID No: 6157035CB1"
	Query Match Best Local Similarity Matches 1091; Conservative	61.2%; Score 1030; DB 6; 98.6%; Pred. No. 8.7e-256; 0; Mismatches 10; Indels 5; Gaps 5;
OY	157 GTGACCTTCCCAAGATAGTCGTGGCGCACATAATCCTCAGGAATTCCCTTGCGATCCTAATAG	216
Dd	367 GTAAGTTGCCAAAGATATGCCTGGCCACAATACTCCAGAAGATTCCCTTGCGATCCTAATAG	426
OY	217 TGAACCCCCCATTAATCAGCCTCTAATTCAATAGTGTCTTATTTGGCGGGCTGTGGGTGTCA	276
Dd	427 TGACACCACCACTTAATCAGCCTCTAATTCATAGTGTCTTATTTGGCGGGCTGTGGGTGTCA	486
OY	277 TTTCGATCTTTCTCTCCGTGGTGA AAAATG AACCCC GGTCAGTAGACACACANNGGCGGTCA	336
Dd	487 TTTCGATCTTTCTCTCCGTGGTGA AAAATG AACCCC GGTCAGTAGACACACANNGGCGGTCA	546
OY	337 TTTAACTTGGNIGTGTCCACAGACGTTTTTCTGTGACAGTGCSCAATTCGCTGTGACCTAAC	396
Dd	547 TTTAACTTGGNIGTGTCCACAGACGTTTTTCTGTGACAGTGCSCAATTCGCTGTGACCTAAC	606
OY	397 TCATCAGAAAGACTTGATGTTTGGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGTGC	456
Dd	607 TCATCAGAAAGACTTGATGTTTGGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGTGC	666
OY	457 ACATCCACATGTACTCA CGTTCTCTATTCATATGAGTGATCTGTGTCACCAAGATACCTCA	516
Dd	667 ACATCCACATGTACTCA CGTTCTCTATTCATATGAGTGATCTGTGTCACCAAGATACCTCA	726
OY	517 TCTTTCTTCAGATGCA AAGCAAAGATGGAATCTTACAGAAAATCTGATCTGTGCTGCGCA	576
Dd	727 TCTTTCTTCAGATGCA AAGCAAAGATGGAATCTTACAGAAAATCTGATCTGTGCTGCGCA	786
OY	577 GTGCTGCGATGTGACGCTGTGATTTGTCAATGTGTGTACCCCTGAGTGTCTCCCGATAG	636
Dd	787 GTGCTGCGATGTGACGCTGTGATTTGTCAATGTGTGTACCCCTGAGTGTCTCCCGATAG	846
OY	637 GAATCCATGAGGAATPACATAGAGAGACGCTTTTAATTTCA AAAGAGCTTGTCTTACA	696
Dd	847 GAATCCATGAGGAATPACATAGAGAGACGCTTTTAATTTCA AAAGAGCTTGTCTTACA	906
OY	697 CATATGTGA AATCATCACTATATATGATGATCTTTTGTATAGCCGTTGCTGTGATTC	756
Dd	907 CATATGTGA AATCATCACTATATGATGATCTTTTGTATAGCCGTTGCTGTGATTC	966
OY	757 TGTGTGTCTTCAGAGCTTCTCATCTATATGTTGATGTGACAGAACTACGCCACTCTTTAC	816
Dd	967 TGTGTGTCTTCAGAGCTTCTCATCTATATGTTGATGTGACAGAACTACGCCACTCTTTAC	1026
OY	817 TAATCCACAGGAATTTCTGGGCTCAGCTGAAAACTATTTTTTNATAGGGTCAATCCTTG	876
Dd	1027 TAATCCACAGGAATTTCTGGGCTCAGCTGAAAACTATTTTTTNATAGGGGTCATCCTTG	1086
OY	877 TTGTGTTCCTTCCCTACAGATTTCTTAAGSATCTTATCTTGAATGTTGTGACGATTTCCA	936
Dd	1087 TTGTGTTCCTTCCCTACAGATTTCTTAAGSATCTTATCTTGAATGTTGTGACGATTTCCA	1146
OY	937 ATG CCTGTAG CAGCAGAGGTG CATTTTATACGAATCTTCTTGAGTGTACAGCAATTYA	996
Dd	1147 ATG CCTGTAG CAGCAGAGGTG CATTTTATACGAATCTTCTTGAGTGTACAGCAATTYA	1206
OY	997 GCTGCTATGATTTGCTTCTCTTTGTCTTTTGGGGGAAGCCATTTGTTTATAGCAAAAGATTA	1056
Dd	1207 GCTGCTATGATTTGCTTCTCTTTGTCTTTTGGGGGAAGCCATTTGTTTATAGCAAAAGATTA	1266
OY	1057 TTG C CTATAGGAATTTGGTTTTTGGGCGTTATAGCCAAACATCAAGTATTCATATTTGGCTT	1116
Dd	1267 -TTG C CTATAGGAATTTGG- TTTTGGCGGTTATAGCCAAACATCAAGTATTCATATTTGGCTT	1324
OY	1117 CCCTTATATTTGGGANT-AAATGGGATATAGGGGAGTATAGATATGATATTTCAATTACTTGA	1175

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Db 1325 CCTTATATGGGAATAAATAGGATAGGGAGGTAAAGATGATATTCTACTTGA 1384
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Qy 1176 TCAAAACATGCTTGAATGATACCCAAAACAAAGACATATAATGCAAGCCCTCAT 1235
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Db 1385 TC-AAAGCATGCTTGAATGATACCCAAAACAAAGACATAT-AAATGCAAGCCCTCAT 1442
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Qy 1236 GTAGTCTTATGGGATCCCTCCCATC 1261
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Db 1443 GTAGTCTTATGGGATCCCTCATCTC 1468
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RESULT 10
AX453412 1051 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 1 from Patent WO0244212.
AX453412
VERSION AX453412.1 GI:21712725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Deleersnijder, W., Blockx, H. and de Moor, L.
AUTHORS Human g-protein coupled receptor and uses thereof
TITLE Patent: WO 0244212-A 1 06-JUN-2002;
JOURNAL SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
source location/Qualifiers
1..1051
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/db_xref="taxon:9606"
60..977
/note="unnamed protein product"
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/db_xref="GI:21712726"
/translation="MPGHNTSRNSCCPIYTPHLISLYFVLIGLVISILFLVYK
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FLFYVILVTRYLLFKCKDKVEFYRLKLVAVASAGMTLVIVLVVSRGISHH
YNEBHCFFKHELAIVTVKILINMIIVFLAVAVAILLVQVFIIMLVQKRLSHLSH
QEFPAOKNLFPIGIVLPCFPLPYOFPIRYLVAVNTVTHSNACNSKAPFNEIFLSTVLAIS
CYDLLLVFPGSHWFKKIKITIGMNCVLCR"
ORIGIN
Query Match 58.9%; Score 991.2; DB 6; Length 1051;
Best Local Similarity 99.6%; Pred. No. 9.8e-246;
Matches 1004; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 155 ATGTGACTTCCCAAGTATGCTTGGCCCAATACCTCCAGAAATTCCTTGGCATCTAT 214
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Db 44 AGGTGACTTCCCAAGTATGCTTGGCCCAATACCTCCAGAAATTCCTTGGCATCTAT 103
|||
Qy 215 AGTGACACCCCACTTATAGCCCTCTACTATGCTTATTTGGCCGGGCTGGGGGCT 274
|||
Db 104 AGTGACACCCCACTTATAGCCCTCTACTATGCTTATTTGGCCGGGCTGGGGGCT 163
|||
Qy 275 CATTTCATCTTCTCTCTGCTGTGAATAAACAACCGGTCAGTGAACAACATGAGGCT 334
|||
Db 164 CATTTCATCTTCTCTCTGCTGTGAATAAACAACCGGTCAGTGAACAACATGAGGCT 223
|||
Qy 335 CATTTCATCTTCTCTCTGCTGTGAATAAACAACCGGTCAGTGAACAACATGAGGCT 394
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Db 224 CATTTCATCTTCTCTCTGCTGTGAATAAACAACCGGTCAGTGAACAACATGAGGCT 283
|||
Qy 395 CCTCATCAAGAAGCTTGAAGTTTGGGCGCCCTTCGCAAAATTTTGGAGTGCAGGCT 454
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Db 284 CCTCATCAAGAAGCTTGAAGTTTGGGCGCCCTTCGCAAAATTTTGGAGTGCAGGCT 343
|||
Qy 455 GCACATCCACATGATCTCAAGTCTTATCTATGATGATGATCTTGGTCAACAGATACCT 514
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Db 344 GCACATCCACATGATCTCAAGTCTTATCTATGATGATGATCTTGGTCAACAGATACCT 403
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Qy 515 CATCTCTTGAAGNCAAGCAAGAGGAATCTACAGAAAACCTGCATGCTGNGGCTC 574
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Db 404 CATCTCTTGAAGNCAAGCAAGAGGAATCTACAGAAAACCTGCATGCTGNGGCTC 463
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Qy 575 CAGTCTGAGCATGAGACGCTGGTGAATTCATTTGNGTACCCCTGGTGTCTCCCGTA 634
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Db 464 CAGTCTGAGCATGAGACGCTGGTGAATTCATTTGNGTACCCCTGGTGTCTCCCGTA 523
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Qy 635 TGGATTCATGAGGAATACATGAGAGCATGTTTTAAATTTACAAAGACTTGTCTTA 694
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Db 524 TGGATTCATGAGGAATACATGAGAGCATGTTTTAAATTTACAAAGACTTGTCTTA 583
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Qy 695 CACATATGNAANAATCATCAATATATGATAGATCATTTTGTCTATAGCCGTGTGAT 754
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Db 584 CACATATGNAANAATCATCAATATATGATAGATCATTTTGTCTATAGCCGTGTGAT 643
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Qy 755 TCTGTGTCTTCCAGGCTCTTCATCATTTATGATGATGATGATGATGATGATGATGAT 814
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Db 644 TCTGTGTCTTCCAGGCTCTTCATCATTTATGATGATGATGATGATGATGATGATGAT 703
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Qy 815 ACTATCCACACAGAGTTCGTGGCTCAGCTGAATAAACTATTTTATAGGGGTCTCT 874
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Db 704 ACTATCCACACAGAGTTCGTGGCTCAGCTGAATAAACTATTTTATAGGGGTCTCT 763
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Qy 875 TGTGTGTCTTCTTCCCTACAGATTCCTTATGATATCTATCTGAAATGTGTGACGATTC 934
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Db 764 TGTGTGTCTTCTTCCCTACAGATTCCTTATGATATCTATCTGAAATGTGTGACGATTC 823
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Qy 935 CAATGCTGTAGACAGAGTTCATTTTATGAAGAACTCTTGAAGTAAACAGCAAT 994
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Db 824 CAATGCTGTAGACAGAGTTCATTTTATGAAGAACTCTTGAAGTAAACAGCAAT 883
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Qy 995 TAGCTGTATGATTTGCTTCTTGTCTTTGGGGAAGCAATGTTTAAAGAAAAGAT 1054
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Db 884 TAGCTGTATGATTTGCTTCTTGTCTTTGGGGAAGCAATGTTTAAAGAAAAGAT 943
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Qy 1055 AATTGGCTTATGGAATTTGTTTGGCCGTATGACCAAACTACAGATTCATTTATTC 1114
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Db 944 AATTGGCTTATGGAATTTGTTTGGCCGTATGACCAAACTACAGATTCATTTATTC 1003
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Qy 1115 TTCCCTTATATATGGAAT-AAATAGGATATAGGGAGGTAAAGATGCT 1161
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Db 1004 TTCCCTTATATATGGAATAAATAGGATATAGGGAGGTAAAGATGCT 1051
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RESULT 11
CQ737895 1332 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 23829 from Patent WO02068579.
CQ737895
VERSION CQ737895.1 GI:42337355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
AUTHORS Kitz, such as nucleic acid arrays, comprising a majority of
TITLE humanexons or transcripts, for detecting expression and other uses
JOURNAL thereof
PATENT: WO 02068579-A 23829 06-SEP-2002;
PE CORPORATION (NY) (US)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 55.2%; Score 930.4; DB 6; Length 1332;
Best Local Similarity 99.9%; Pred. No. 5.8e-230;

QY	831	TTCTGGGGCTCACTGAAAAAACCCTATTTTTTATAGGGGGTCATCCCTGTTGTTGCTCC	890
Db	661	TTCTGGGGCTCACTGAAAAAACCCTATTTTTTATAGGGGGTCATCCCTGTTGTTGCTCC	720
QY	891	TACCAAGTCTTGTAGGAGTCTATTAATGTTGATGTTGAGCGCATTCGAATGCTGTGACGC	950
Db	721	TACCAAGTCTTGTAGGAGTCTATTAATGTTGATGTTGAGCGCATTCGAATGCTGTGACGC	780
QY	951	AAGGTTCATTTTATPAAGAAATCTTCTTGAGTGTAAACAGCAATTAAGTGTATGATTTG	1010
Db	781	AAGGTTCATTTTATPAAGAAATCTTCTTGAGTGTAAACAGCAATTAAGTGTATGATTTG	840
QY	1011	CTTCTCTTGTCTTTGGGGGAAAGCAATGTTTAAAGCAAAATTAATGGCTATAGAAAT	1070
Db	841	CTTCTCTTGTCTTTGGGGGAAAGCAATGTTTAAAGCAAAATTAATGGCTATAGAAAT	900
QY	1071	TGTGTTTGTGCGCGTTAG 1088	
Db	901	TGTGTTTGTGCGCGTTAG 918	
RESULT 13			
LOCUS	AX481576	918 bp	DNA
DEFINITION	Sequence 1 from Patent EP1225183.	linear	PAT 16-AUG-2002
ACCESSION	AX481576		
VERSION	AX481576.1	GI:22316490	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
TITLE	Harland, L.		
JOURNAL	Human g-protein coupled receptor Patent: EP 1225183-A 1 24-JUL-2002; Pfizer Limited (GB) ; PFIZER INC. (US)		
FEATURES	Location/Qualifiers		
source	1..918		
ORIGIN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
Query Match	54.4%; Score 916.4; DB 6; Length 918;		
Best Local Similarity	99.9%; Pred. No. 2.4e-226;		
Matches 917; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY	171	ATGCTGGCCACATATCTCCAGCAATTCCTCTTGCGATTCCTATAGTACACCCCACTTA	230
Db	1	ATGCTGGCCACCAATACCTCCAGCAATTCCTCTTGCGATTCCTATAGTACACCCCACTTA	60
QY	231	ATCAGCCCTCTATCTGATAGTGCCTTATTTGGCGGGCGTGGGGGTGATTTCCATTCCTTTC	290
Db	61	ATCAGCCCTCTATCTGATAGTGCCTTATTTGGCGGGCGTGGGGGTGATTTCCATTCCTTTC	120
QY	291	CTCCTGTGAATAATGACACCCCGGTCACTGATGACACATAGCGGTCAATTAATTGGTGGTG	350
Db	121	CTCCTGTGAATAATGACACCCCGGTCACTGATGACACATAGCGGTCAATTAATTGGTGGTG	180
QY	351	GTCACAGCGTTTTTCTGCTGACAGTGCACATTTGGCTTGAACCTTCATCAAGAAAGCT	410
Db	181	GTCACAGCGTTTTTCTGCTGACAGTGCACATTTGGCTTGAACCTTCATCAAGAAAGCT	240
QY	411	TGAGATGTTGGGCGCCCTTCTGCAAAATTTGGAGTGCATGTCACATCAATGATAC	470
Db	241	TGAGATGTTGGGCGCCCTTCTGCAAAATTTGGAGTGCATGTCACATCAATGATAC	300
QY	471	CTCAAGTCTATTTCTATGTATGTATCTCTGTCACAGATACATCTTCTTCAAGTGC	530
Db	301	CTCAAGTCTATTTCTATGTATGTATCTCTGTCACAGATACATCTTCTTCAAGTGC	360
QY	531	AAAGCAAAAGTGAATTTCTACAGAAAACTGTAGCTGTGCTGCACAGTGTGGATGCG	590

Db	Sequence	Score	DB	Length	Indels	Gaps
Db	AAAGCAAAGTGAATTCACAGAAACATGATCTGTGGTGCAGTGTGGCAATGGG 420					
Qy	ACGGTGTGATTTGATCTATTTGGTACCCCTGGTTGTCTCCGGTATNGAATCATAGAGAA 650	54.4*		918	0	0
Db	ACGGTGTGATTTGATCTATTTGGTACCCCTGGTTGTCTCCGGTATNGAATCATAGAGAA 480					
Qy	TACATATGAGAGCACTGTTTAAATTTACAAAGAGCTTGCTTACATATGTGAAATC 710					
Db	TACATATGAGAGCACTGTTTAAATTTACAAAGAGCTTGCTTACATATGTGAAATC 540					
Qy	ATCAACTATATGATATGATCTTTTGTCTATAGCCGTGCTGTGATTTCTGTGGTCTTCCAG 770					
Db	ATCAACTATATGATATGATCTTTTGTCTATAGCCGTGCTGTGATTTCTGTGGTCTTCCAG 600					
Qy	GCTTTCATCATTTATGTTGATGTGTCAGAGCTACGCCACTCTTACTATCCACAGAG 830					
Db	GCTTTCATCATTTATGTTGATGTGTCAGAGCTACGCCACTCTTACTATCCACAGAG 660					
Qy	TTCTGGGCTCAGCTGAAACCTTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCC 890					
Db	TTCTGGGCTCAGCTGAAACCTTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCC 720					
Qy	TACAGATTTTATGATCTATTTACTTGAATGTTGTGACATTTCCATATGCTGTAGACG 950					
Db	TACAGATTTTATGATCTATTTACTTGAATGTTGTGACATTTCCATATGCTGTAGACG 780					
Qy	AAGGTGCATTTTATACGAATCTTCTGTAGTGTACAGCAATTTAGCTGTATGATTTG 1010					
Db	AAGGTGCATTTTATACGAATCTTCTGTAGTGTACAGCAATTTAGCTGTATGATTTG 840					
Qy	CTTCTCTTTTGTCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATATTTGGCTTATGGAAT 1070					
Db	CTTCTCTTTTGTCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATATTTGGCTTATGGAAT 900					
Qy	TGTGTTTGTGTCCTGTAG 1088					
Db	TGTGTTTGTGTCCTGTAG 918					
RESULT 14						
AX498180						
LOCUS	AX498180 918 bp DNA linear PAT 26-SEP-2002					
DEFINITION	Sequence 3 from Patent WO242461.					
ACCESSION	AX498180					
VERSION	AX498180.1 GI:234343111					
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
JOURNAL	Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.					
FEATURES	Endogenous and non-endogenous versions of human g protein-coupled					
source	Patent: WO 0242461-A 3 30-MAY-2002;					
	Arena Pharmaceuticals, Inc. (US)					
	location/Qualifiers					
	1. 918					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
Query Match	54.4*; Score 916.4; DB 6; Length 918;					
Best Local Similarity	99.9%; Pred. No. 2,4e-226;					
Matches 917; Conservative	0; Mismatches 1; Indels 0; Gaps 0;					
Qy	ATGCGCTCTAATCTCATAGTACTTATTTGGGGGCTGGTGGGTGTCAATTTCCATTTCTTTTC 230					
Db	ATGCGCTCTAATCTCATAGTACTTATTTGGGGGCTGGTGGGTGTCAATTTCCACTTTA 60					
Qy	ATGCGCTCTAATCTCATAGTACTTATTTGGGGGCTGGTGGGTGTCAATTTCCACTTTTC 290					

Db		61	ATCAGCCTCTCATCTGATATGCTTATTTGGCGGGCTGGTGGGTGTCATTTCCATTTCTTTTC	120
Oy		291	CTCCTGTGAAAATGAAACACCCGGTCACTGACCAACATGAGGGGTCAATTAACTTGGTGTG	350
Db		121	CTCCGTGGTAAATATGAACACCCGGTCACTGACCAACATGAGGGGTCAATTAACTTGGTGTG	180
Oy		351	GTCCACAGCGTTTTTCTGTGTGACAGTGCATTTTGGCTTGAACCTTACCTCATCAAGACACT	410
Db		181	GTCCACAGCGTTTTTCTGTGTGACAGTGCATTTTGGCTTGAACCTTACCTCATCAAGACACT	240
Oy		411	TGGATGTTTGGGCTGCCCTCTCGCAAAATTTGTAGTGTGCATGCTGCACATCCATGATGAC	470
Db		241	TGGATGTTTGGGCTGCCCTCTCGCAAAATTTGTAGTGTGCATGCTGCACATCCATGATGAC	300
Oy		471	CTCAGCTTCTATTTCTATGTAGTGTGATCTCCGTGTACACAGATACCTCATCTTCTGAAGTGC	530
Db		301	CTCAGCTTCTATTTCTATGTAGTGTGATCTCCGTGTACACAGATACCTCATCTTCTGAAGTGC	360
Oy		531	AAAGCAAAAGTGGAAATTTTACAGAAAATCTGATGTGTGTGCTGCCAGTGTCTGGCATGTGG	590
Db		361	AAAGCAAAAGTGGAAATTTTACAGAAAATCTGATGTGTGTGCTGCCAGTGTCTGGCATGTGG	420
Oy		591	AAGCGTGGATTTGTATCTAGTGTGTGATCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA	650
Db		421	AAGCGTGGATTTGTATCTAGTGTGTGATCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA	480
Oy		651	TACATATGAGAGACACTGTTTTTAAATTTTCACAAAGACTTGTGCTTACATATGTGAAAAATC	710
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Oy		711	ATCAAATATATGATATGATCATTTTTTGTGTACAGCCGTTGCTGTGATTTCTGTTGTCCTGAG	770
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Oy		771	GTCCTTCATCATTTATGCTTGTATGTGTGAGAAAGCTAGGCCACTCTTATATATCCACAGAGAG	830
Db		601	GTCCTTCATCATTTATGCTTGTATGTGTGAGAAAGCTAGGCCACTCTTATATATCCACAGAGAG	660
Oy		831	TTCTGGGGCTCAGCTGAAAACCTATTTTTTTATAGGGGGTATCTGTTGTTTCTTCTCC	890
Db		661	TTCTGGGGCTCAGCTGAAAACCTATTTTTTTATAGGGGGTATCTGTTGTTTCTTCTCC	720
Oy		891	TACCAAGTCTTATAGAGTATATTACTTGTAGATGTTGTGACGATTCGAATCCAGTCTGTAGCAGC	950
Db		721	TACCAAGTCTTATAGAGTATATTACTTGTAGATGTTGTGACGATTCGAATCCAGTCTGTAGCAGC	780
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Oy		1071	TGTGTTTGTGCGCTTAG	1088
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LOCUS				
BD105324				
DEFINITION				
Novel G protein-coupled receptor protein and its DNA.				
ACCESSION				
BD105324.1 GI:22650898				
VERSION				
BD105324.1 GI:22650898				
KEYWORDS				
WO 0196567-A/1.				
SOURCE				
Homo sapiens (human)				
ORGANISM				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE				
1 (bases 1 to 918)				
Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.				

Query Match	Best Local Match	Similarity	Score	DB	Length	Key			
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FEATURES									
source									
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Location/Qualifiers									
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/organism='Homo sapiens'									
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/db_xref='taxon:9606'									
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Best Local Match									
Similarity									
Score									
DB									
Length									
Key									
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1	ATGCTGTGGCCACCAATACCTCCAGGAATTCCTTTGCGATTCCTATAGTACACCCCACTTA	60							
231	ATCAGCCTCTAATTCATATGCTCTTATTTGGGGGGCTGGTGGGTGTCATTTCCATTCTTTTC	290							
61	ATCAGCCTCTAATTCATATGCTCTTATTTGGGGGGCTGGTGGGTGTCATTTCCATTCTTTTC	120							
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121	CTCCTGTGGAATAAGAACACCGGTCAGTGCACACATGGGGGTCATTAACTTTGGTGGTG	180							
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241	TGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGTGCATGCTGCACATCCACATGTAC	300							
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301	CTCAGGTTCCATTCATATGCTGTATCCTGTGTCACAGATACCTCATCTTCTTCAAGTGC	360							
531	AAAGCAAAAGTGAATTCACAGAAACCTGCATGTGTGGCTGCCAGTCTGCAGATGTGG	590							
361	AAAGCAAAAGTGAATTCACAGAAACCTGCATGTGTGGCTGCCAGTCTGCAGATGTGG	420							
591	ACGCTGTGATTTGTCATTTGTGTACCCCTGGTTGTCTCCGGTATGAATTCATGAGGAA	650							
421	ACGCTGTGATTTGTCATTTGTGTACCCCTGGTTGTCTCCGGTATGAATTCATGAGGAA	480							
651	TACAAATGAGGACCTGTTTAAATTTCAAGAAAGCTTGTTACATATGTGAATTC	710							
481	TACAAATGAGGACCTGTTTAAATTTCAAGAAAGCTTGTTACATATGTGAATTC	540							
711	ATCAACTATATGATAGTCAATTTTGTCAATACCGCTGTGTGATTTCTTGGTCTTCAG	770							
541	ATCAACTATATGATAGTCAATTTTGTCAATACCGCTGTGTGATTTCTTGGTCTTCAG	600							
771	GTCCTCATCATTAATGTTGATGTGTGCAAGGTCACCACTCTTTAATATCCACCAAGAG	830							

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Db      601  GTCTTCATCATTAATGTTGATGATGCGAAGCTACGCCACTCTTTACTATCCACACGAGG 660
Qy      831  TTCTGGGCTCAGCTGAATAACCTATTTTATAGGGGTCAATCCTTGTGTTTCTTCC 890
Db      661  TTCTGGGCTCAGCTGAATAACCTATTTTATAGGGGTCAATCCTTGTGTTTCTTCC 720
Qy      891  TACCAATCTTTAGGATCTATTAATGTAATGTTGACGCAATCCCAATGCCGTAGCAGC 950
Db      721  TACCAATCTTTAGGATCTATTAATGTAATGTTGACGCAATCCCAATGCCGTAGCAGC 780
Qy      951  AAGTTGATTTTATTAAGAAATCTTCTGAGTGTAAACAGCAATTAGCTGCTATGATTTG 1010
Db      781  AAGTTGATTTTATTAAGAAATCTTCTGAGTGTAAACAGCAATTAGCTGCTATGATTTG 840
Qy      1011 CTTCCTTTGCTTTGGGGGAAGCCATGTTTAAAGCAAAAGATTAATGGCTATGGAAT 1070
Db      841  CTTCCTTTGCTTTGGGGGAAGCCATGTTTAAAGCAAAAGATTAATGGCTATGGAAT 900
Qy      1071 TGTGTTTGTGCCGTTAG 1088
Db      901  TGTGTTTGTGCCGTTAG 918
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Search completed: September 10, 2005, 07:21:29
Job time : 7576.62 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:42:15; Search time 981.638 Seconds
(without alignments)
10155.318 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseg2003bs:*
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12: geneseg2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1683	99.9	1684	6	AAL53413 1684 nt c
2	1472.6	87.4	2525	4	AAB51009 Human ncp
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4	1472.2	87.4	113306	10	ADCB6554 Human GPC
5	1228.6	73.0	1336	6	AAAF88583 Human GCR
6	1106.2	65.7	1340	6	AAAF88584 Human GCR
7	1106.2	65.7	1460	6	AAAF88585 Human GCR
8	1030	61.2	1499	6	AAD37670 Human G-P
9	991.2	58.9	1051	6	ABK87351 Human G-P
10	968	57.5	1040	9	AAAL57070 Human G-P
11	939	55.8	939	6	AAAL53414 939 nt co
12	916.4	54.4	918	6	AAAL44713 Human tes
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17	913.4	54.2	1632	10	ADPF0589 Orphan re
18	690	41.0	972	10	ADCI2789 Human GPC
19	636.8	37.8	1170	10	AD121991 Novel hum
20	634.8	37.7	918	12	AD028921 Mouse nov

ALIGNMENTS

21	559.2	33.2	810	10	ADB78584	ADB78584 Mouse G-P
22	404.4	24.0	447	6	AAB50979	AAB50979 Human ncp
C 23	404.4	24.0	447	6	AB570212	AB570212 DNA encod
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26	144.8	8.6	897	10	AB223663	AB223663 G protein
27	76.4	4.5	1113	5	AB198010	AB198010 Non-endog
28	76.4	4.5	1805	6	AB553446	AB553446 CDNA enco
29	76.4	4.5	1829	10	ABX94264	ABX94264 Human orp
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31	76.4	4.5	1829	10	ABX94263	ABX94263 Human orp
32	76.4	4.5	1973	10	ADCA0517	ADCA0517 DNA deriv
33	76.4	4.5	1973	10	ACA56793	ACA56793 Human sig
34	76.4	4.5	1973	11	AD132091	AD132091 Human cdn
35	76.4	4.5	1973	12	AD156589	AD156589 Human pol
36	76.4	4.5	2534	8	AB242709	AB242709 Human opi
37	76.4	4.5	2534	10	ABX94045	ABX94045 CDNA enco
38	76.4	4.5	2534	10	ADK52573	ADK52573 Hematolog
39	76.4	4.5	2534	12	AD030012	AD030012 Human GPC
40	76.4	4.5	2534	13	ADQ88235	ADQ88235 Human 261
41	76.4	4.5	3205	12	ADL12442	ADL12442 Human ste
42	76.4	4.5	3330	12	ADQ24525	ADQ24525 Human sof
43	74.8	4.4	1829	10	ABX94260	ABX94260 Human orp
44	73.2	4.3	1134	3	AAZ60659	AAZ60659 DNA encod
45	71.6	4.3	1334	12	ADM67099	ADM67099 Murine ad

RESULT 1

AAL53413
ID AAL53413 standard; CDNA; 1684 BP.

AC AAL53413;

DT 12-DEC-2002 (first entry)

DE 1684 nt cDNA of human G-protein coupled receptor type protein.

XX Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory;
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
XX antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
XX cardiant; dermatological; antinfertility; hepatotropic; antiallergic;
XX antispasmodic; ophthalmological; antianaginal; antihypoid; anticonvulsant;
XX antineumatic; antiarthritic; G-protein coupled receptor; subfamily I;
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;
XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
XX cellular proliferative; differentiative disorder; hormonal disorder;
XX neurological disorder; cardiovascular disorder; viral disease; pain;
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
XX viral meningitis; fungal meningococcalitis; multiple sclerosis;
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
XX Huntington's disease; heart failure; angina pectoris; dermatitis;
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
XX transgenic animal; human; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 147..1088
XX FT /*tag= a
XX FT /product= "Human G-protein coupled receptor type protein
XX 93870"

XX MO200270657-A2.

XX 12-SEP-2002.

XX 28-FEB-2002; 2002W0-US006455.

XX 01-MAR-2001; 2001US-0272677P.
PR (MILL-) MILLENNIUM PHARM INC.
PA Glucksmann MA;
XX WPI; 2002-732793/79.
DR P-PSDB; AAO22919.
XX
FT New G-protein coupled receptor used in receptor assays as a target for
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT disorders.
XX
PS Claim 5; Page 99-100; 105pp; English.
XX
CC The invention relates to an isolated polypeptide, which is a G-protein
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
CC receptor type proteins (GPCRs), designated the 93870 receptor. The
CC polypeptides, nucleic acid molecules and antibodies of the invention are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC monitoring clinical trials or pharmacogenetics), or in methods of
CC treatment (e.g. therapeutic and prophylactic). They are useful in
CC treating and diagnosing conditions related to aberrant activity or
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC disorders, or bone marrow mononuclear disorders, as well as cellular
CC proliferative and/or differentiative disorders, hormonal disorders,
CC neurological disorders, cardiovascular disorders, viral diseases, liver
CC disorders, and pain and metabolic disorders. Conditions that can be
CC treated include cancer, diabetes mellitus, hypothyroidism,
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC viral meningitis, fungal meningoenephalitis, multiple sclerosis,
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC Huntington's disease, heart failure, angina pectoris, myocardial
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC transgenic animals are useful for studying the function and/or activity
CC of a 93870 protein and for identifying and/or evaluating modulators of
CC 93870 activities. The polynucleotides of the invention can be used in
CC gene therapy. This polynucleotide sequence represents the cDNA of the
CC 1684 nucleotide human G-protein coupled receptor type protein of the
CC invention
XX
SQ Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;
Query Match 99.9%; Score 1683; DB 6; Length 1684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 TCGAAGTTGTAGATCGATTAAGAGATGCTCACTAAGGAGATTCCTGATGCGCTTTAGA 120
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DB 301 AAATGAACACCGGTCACTGACCAACCATGGGGGTATTAACTTGGTGTGTCACACGCG 360
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DB 361 TTTTTCGTGACAGAGGCCATTTCCGTGACCTAATCTATCAAGAAAGCTTGGATGTTGG 420
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DB 481 TATTTATATGTGTATCTGATCTGATCCACAGATACCTCATCTTTCGAAGTGCAGAAAG 540
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DB 721 TGATATGATTTTTTGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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QY 1021 TCTTTGGGGAGAGCCATTTGTTTAAAGCAAAAAGTAAATGCTTATGGAATTTGTTTGT 1080
DB 1021 TCTTTGGGGAGAGCCATTTGTTTAAAGCAAAAAGTAAATGCTTATGGAATTTGTTTGT 1080
QY 1081 GCGGTATGCCAACAATCTAGATATCATATTTGCTCTTATATATGGAATTAATATGGG 1140
DB 1081 GCGGTATGCCAACAATCTAGATATCATATTTGCTCTTATATATGGAATTAATATGGG 1140
QY 1141 TATATGGGAGGTAAAGATGATTTTCACTTATCTGATCAAAACCATGCTTATGATGACCA 1200
DB 1141 TATATGGGAGGTAAAGATGATTTTCACTTATCTGATCAAAACCATGCTTATGATGACCA 1200
QY 1201 AAACAAAAGACTAATAAATGCAAGAGCCCTCATTTGATGCTTATATGGAATTCCTCCAT 1260
DB 1201 AAACAAAAGACTAATAAATGCAAGAGCCCTCATTTGATGCTTATATGGAATTCCTCCAT 1260
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Db 609 ATTCTGTGGTCTTCCAGGCTTTCATCATATATGTTAGTGCGAAGCTACGCCACTCT 668
Qy 813 TTACTATCCACGAGAGGTTGCGGCTCAGCTGAAAAACCAATTTTATATAGGGGCTATC 872
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Qy 873 CTGTGTGTGTTCCCTTCCCTACAGGCTCTTAAAGATATATATCTTGAATGTTGTAGCCAT 932
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Qy 1053 ATAAATGGCTTATGGAATTTGTTTGTGCGGTTAGCCACAACTACAGTATTCATATTT 1112
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Qy 1113 GCTTCCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGGTATTTTCATTAC 1171
Db 969 GCTTCCTTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAAGGTATTTTCATTAC 1028
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Qy 1352 CCCATGAAGAACAATAGTATTTAAGATTTTAAAGATTTTAAAGCTCATTTCAAGTTC 1411
Db 1209 CCCATGAAGAACAATAGTATTTAAGATTTT-AGAGTTTATTAAGCTCATTTCAAGTTC 1267
Qy 1412 CTCTGTGTGAAGCATGCTCTCTTAAGTTTGGACTGAACTGACACTTTAGTCTTTTCA 1471
Db 1268 CTCTGTGTGAAGCATGCTCTCTTAAGTTTGGACTGAACTGACACTTTAGTCTTTTCA 1327
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Db 1328 TCCCATCTACCAATAGTAAATTAATCTGGCCACACCCAGCTCCAAAGACAAATC 1387
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Db 1388 TCCTTGTGTAACCAAGTATAGTCCCATTCATCTCATGCTCCGTAATAAACTGATAAG 1447
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Qy 1652 AGA 1654
Db 1508 AGA 1510
```

RESULT 3
ABST0242
ID ABST0242 standard; DNA; 2525 BP.
XX
AC ABST0242;

```
XX 26-NOV-2002 (first entry)
DT
XX
XX DNA encoding human G protein-coupled receptor, nGPR-16.
DE
XX Human; gene; ds; G protein-coupled receptor; GPCR; nGPR; beGPR;
KW nGPR protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.
XX
OS Homo sapiens.
XX
XX W0200264789-A1.
XX
XX 22-AUG-2002.
XX
XX 14-FEB-2001; 2001MO-US004641.
XX
XX 14-FEB-2001; 2001MO-US004641.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Parodi LA, Vogel G, Wood LS;
XX
XX WPI, 2002-674879/72.
XX
XX P-PSDB; ABG93787.
XX
XX
XX New nucleic acids and polypeptides of the ng protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
XX Example 1; Page 84-85; 244pp; English.
XX
XX The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC ng protein coupled receptor-14 (nGPR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nGPR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder
CC and for identifying a compound useful as a modulator of binding between
CC nGPR-14 and a binding partner of nGPR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesia, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABST0202-ABST0248, ABST0338 and ABST0243 are the DNAs
CC encoding the nGPRs (also referred to as beGPCRs)
XX
XX
SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;
```

Query Match 87.4%; Score 1472.6; DB 6; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

```
Qy 153 AATGTACTTCCCAAGTATAGCTGGCCACAAATACCTCCAGAAATCTCTTGGAGCTT 212
Db 9 ACAAGTACTTCCCAAGTATAGCTGGCCACAAATACCTCCAGAAATCTCTTGGAGCTT 68
```


213 ATAGTACACCCCACTTATACAGCTCTACTTATCATAGTGTCTTATTTGGCGGGCTGGTGGGT 272
 69 ATAGTACACCCCACTTATACAGCTCTACTTATCATAGTGTCTTATTTGGCGGGCTGGTGGGT 128
 273 GTCAATTTCAATCTTTTCTCTCTGGTGAATAATGAACACCCGGTCACTGACCAACCAATGGCG 332
 129 GTCAATTTCAATCTTTTCTCTCTGGTGAATAATGAACACCCGGTCACTGACCAACCAATGGCG 188
 333 GTCAATTAATCTTGGTGTGTGTCACAGCGTTTTCCTGTCGACAGTGTCCATTTGCTTGAAC 392
 189 GTCAATTAATCTTGGTGTGTGTCACAGCGTTTTCCTGTCGACAGTGTCCATTTGCTTGAAC 248
 393 TACCTCATCAAGAAGACTTGGATGTTTGGGCTGCGCTTCGCAAAATTTGTGAGTGCATG 452
 249 TACCTCATCAAGAAGACTTGGATGTTTGGGCTGCGCTTCGCAAAATTTGTGAGTGCATG 308
 453 CTGACATCCACATGTATCTTACCGTTCTTATTTCTATGTGTGATCTTGGTCAACAGATAC 512
 309 CTGACATCCACATGTATCTTACCGTTCTTATTTCTATGTGTGATCTTGGTCAACAGATAC 368
 513 CTCAATCTTCTTCAAGTGCAGAAACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCT 572
 369 CTCAATCTTCTTCAAGTGCAGAAACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCT 428
 573 GCCAGTGTGGCATGTGAGCGCTGGTGAATGTCAATGTGTGATACCCCTGGTGTCTCCCGG 632
 429 GCCAGTGTGGCATGTGAGCGCTGGTGAATGTCAATGTGTGATACCCCTGGTGTCTCCCGG 488
 633 TATGGAATCCATGAGGAATATACATGAGAGGACCTGTTTAAATTTCACAAAAGAGCTTGTCT 692
 489 TATGGAATCCATGAGGAATATACATGAGAGGACCTGTTTAAATTTCACAAAAGAGCTTGTCT 548
 693 TACCATATGTGGAATAATCATCACTATATGTATGATCATTTTGTCTATGCGCTGTGTG 752
 549 TACCATATGTGGAATAATCATCACTATATGTATGATCATTTTGTCTATGCGCTGTGTG 608
 753 ATTCTGTGTGTCTTCCAGGTCTTTCATCATATGTTGATGTGAGAGGACCTGCGCACTCT 812
 609 ATTCTGTGTGTCTTCCAGGTCTTTCATCATATGTTGATGTGAGAGGACCTGCGCACTCT 668
 813 TTACTATCCACAGAGGTTCTGGGCTCAGCTGAGAAAACCTATTTTATATAGGGGTCAATC 872
 669 TTACTATCCACAGAGGTTCTGGGCTCAGCTGAGAAAACCTATTTTATATAGGGGTCAATC 728
 873 CTGTGTGTGTCTTCCCTTCCATCCAGTCTTATAGATCTATTAATCTTGAATGTTGTGACGAT 932
 729 CTGTGTGTGTCTTCCCTTCCATCCAGTCTTATAGATCTATTAATCTTGAATGTTGTGACGAT 788
 933 TCCAAATGCTGTAGCAGAGGTTGCAATTTTATACGAATACTTCTTGAAGTGTAAACGACA 992
 789 TCCAAATGCTGTAGCAGAGGTTGCAATTTTATACGAATACTTCTTGAAGTGTAAACGACA 848
 993 ATTAGCTGTATGATTTGCTCTCTTGTCTTTGGGGAGACCAATGGTTTAAACAAAG 1052
 849 ATTAGCTGTATGATTTGCTCTCTTGTCTTTGGGGAGACCAATGGTTTAAACAAAG 908
 1053 ATAAATGGCTTATGGAATGTGTGTTTGTGCGCTTACCAAACTATCAATTCATATTT 1112
 909 ATAAATGGCTTATGGAATGTGTGTTTGTGCGCTTACCAAACTATCAATTCATATTT 968
 1113 GCTTCCTTATATTTGGGAAT-AAAATGGGTATAGGGAGGTAAGAGTATTTTCAATTAC 1171
 969 GCTTCCTTATATTTGGGAATAAAATGGGTATAGGGAGGTAAGAGTATTTTCAATTAC 1028
 1172 TTGATCAAAAACCATGCTTGTATGTACCAAAAACAAAGACTATTAATATGCAAGGCTT 1231
 1029 TTGATCAAAAACCATGCTTGTATGTACCAAAAACAAAGACTATTAATATGCAAGGCTT 1088
 1232 CATGTGTGCTTATATGGGATCCCTCCCATCTCTGTAGTGTGCGGTACAAAGACCAAGTGT 1291
 1089 CATGTGTGCTTATATGGGATCCCTCCCATCTCTGTAGTGTGCGGTACAAAGACCAAGTGT 1148
 1292 TGTGTAATCCACCTGAGGTTGCAATATTAATTTTCCAGTACAGAAATGTCTGTGTGG 1351

1149 TGTGTAATCCACCTGAGGTTGCAATATTAATTTTCCAGTACAGAAATGTCTGTGTG 1208
 1352 CCATGAAAGCAATAGTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTT 1411
 1209 CCATGAAAGCAATAGTTTAAAGATTTT-AGAATTTCAATAGCTCATTTAAAGTTTC 1267
 1412 CTCTGTTTGAAGCATGTCTCTTATGCTTTTGAATGATCTGAATCTGAACCTTTAGTCTTTTCA 1471
 1268 CTCTGTTTGAAGCATGTCTCTTATGCTTTTGAATGATCTGAATCTGAACCTTTAGTCTTTTCA 1327
 1472 TCCCACTTACCATAGGTTAAGTAAATCTGGCCACACCCAGCTCCAAAGACAAATCTC 1531
 1328 TCCCACTTACCATAGGTTAAGTAAATCTGGCCACACCCAGCTCCAAAGACAAATCTC 1387
 1388 TCCTTCCGTAACAGGTTAAGTATGTCCTCATTCATTCATGCGCTGATAAATCTGATTAAGG 1447
 1592 GGAGAGAAATAGTTAAATTTTCTTATGAGTATCTAACTCTGTGTGAGAACTCATCTGTCT 1651
 1448 GGAGAGAAATAGTTAAATTTTCTTATGAGTATCTAACTCTGTGTGAGAACTCATCTGTCT 1507
 1652 AGA 1654
 1508 AGA 1510
 RESULT 4
 ADC86554
 ID ADC86554 standard; DNA; 113306 BP.
 XX
 AC ADC86554;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human GPCR gene SEQ ID NO:1007.
 XX
 KW day; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 OS Homo sapiens.
 XX
 PN BP1270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PE 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 DR WPI; 2003-315783/31.
 DR P-PSDB; ADC86555.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 PS
 PS Claim 1; SEQ ID NO 1007; 28pp; English.
 CC
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.

Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;

Query Match	87.4%	Score 1472.2	DB 10	Length 113306
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Best Local Similarity 99.7%; Pred. No. 0;

Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY	155	ATGGAATTCCTCCAAAGTATGCTGTGGCAAAATACCTCAGAAATTCCTTGTGGATCTAT	214
Db	11524	AGGTGACTTCCCAAGTATGCTGTGGCAAAATACCTCAGAAATTCCTTGTGGATCTAT	115893
QY	215	AGTGAACACCCCACTTAATACGCTCTACTTCAATAGTCTTAATTTGGCGGCTGTGTGTGT	274
Db	11584	AGTGAACACCCCACTTAATACGCTCTACTTCAATAGTCTTAATTTGGCGGCTGTGTGTGT	116433
QY	275	CATTCCATCTTTTCCCTCGGTGTAAATGAACACCGGTGATGACCAACATGGCCGT	334
Db	11644	CATTCCATCTTTTCCCTCGGTGTAAATGAACACCGGTGATGACCAACATGGCCGT	117030
QY	335	CATTAACTTGGTGTGTCCACAGCGTTTTTCTGTGACAGTGCATTTTGGCTTGACCTA	394
Db	11704	CATTAACTTGGTGTGTCCACAGCGTTTTTCTGTGACAGTGCATTTTGGCTTGACCTA	117633
QY	395	CTTCATCAAGAAGACTTGGATGTTTTGGGCTGCGCTTCTGCAATTTGTGTAGTGCATGCT	454
Db	11764	CTTCATCAAGAAGACTTGGATGTTTTGGGCTGCGCTTCTGCAATTTGTGTAGTGCATGCT	118233
QY	455	GCACATCAAGATGATCCTCAGTCTCCATCTATATGTGTGTATCCTGTGTACCAAGATACCT	514
Db	11824	GCACATCAAGATGATCCTCAGTCTCCATCTATATGTGTGTATCCTGTGTACCAAGATACCT	118833
QY	515	CATCTTCTTCAAGTGCAAGACAAAGTGAATTTCAAGAAACTGCAATGCTGTGTGCTGC	574
Db	11884	CATCTTCTTCAAGTGCAAGACAAAGTGAATTTCAAGAAACTGCAATGCTGTGTGCTGC	119433
QY	575	CAGTGTGGGATGTGGACGCTGTGTATGTGCAATTTGTATACCCGTGTGTCTCCCGGTAT	634
Db	11944	CAGTGTGGGATGTGGACGCTGTGTATGTGCAATTTGTATACCCGTGTGTCTCCCGGTAT	120033
QY	635	TGGAATCCATGAGGAATATCAATGAGAGCACTGTTTTAAATTTCACAAAGACTTGTCTTA	694
Db	12004	TGGAATCCATGAGGAATATCAATGAGAGCACTGTTTTAAATTTCACAAAGACTTGTCTTA	120633
QY	695	CACATATGTGAAAAATCATCACTATATGATAGTCAATTTTGTATAGCCGTGTGTGTAT	754
Db	12064	CACATATGTGAAAAATCATCACTATATGATAGTCAATTTTGTATAGCCGTGTGTGTAT	121233
QY	755	TCTGTGTGTCTTCCAGGCTCTTCAATCATATGATGTGTGTGTGTGTGTGTGTGTGTGT	814
Db	12124	TCTGTGTGTCTTCCAGGCTCTTCAATCATATGATGTGTGTGTGTGTGTGTGTGTGTGT	121833
QY	815	ACTATCCACAGGAGTCTTGGGCTCAGCTGA AAAA CTAATTTTTATAGGGGTCACTCT	874
Db	12184	ACTATCCACAGGAGTCTTGGGCTCAGCTGA AAAA CTAATTTTTATAGGGGTCACTCT	122433
QY	875	TGTTTGTTCCTTCCCTACAGTCTCTTATAGATCTATCTTGAATGTGTACCGATTC	934
Db	12244	TGTTTGTTCCTTCCCTACAGTCTCTTATAGATCTATCTTGAATGTGTACCGATTC	123033
QY	935	CAATGCTGTAGCAGCAAGGTTGCATTTTATTAACGAATCTTCTTGAGTGTAAACAGCAAT	994
Db	12304	CAATGCTGTAGCAGCAAGGTTGCATTTTATTAACGAATCTTCTTGAGTGTAAACAGCAAT	123633
QY	995	TAGTGTCTATGATTTGTCTTCTTTTGTCTTTTGGGGGAGCCATTTGTTTAAGCAAAAGAT	1054
Db	12364	TAGTGTCTATGATTTGTCTTCTTTTGTCTTTTGGGGGAGCCATTTGTTTAAGCAAAAGAT	124233
QY	1055	AATGAGCTTATGGAATGTGTTTTGTGTGCGGTGACCAAACTATAGATTTCAATATTGAC	1114
Db	12424	AATGAGCTTATGGAATGTGTTTTGTGTGCGGTGACCAAACTATAGATTTCAATATTGAC	124833
QY	1115	TTCTTTATATTTGGGAAT-AAAATGGGTATAGGGGAGTAAAGATGTATTTCAATTACTT	1173

Dd		12484	TTCCTTTATATTGGGAATAAAAAATGGGTATAGGGAAGGTAAAGAATGTATTCTACTT	12553
Oy		1174	GATCAAAAACCATCCTTGATGTATCCCAAAAACAAAGACTATPAAATGCAGAGCCCTCA	1233
Dd		12544	GATCAAAAACCATCGCTTGATGTATCCCAAAAACAAAGACTATPAAATGCAGAGCCCTCA	12603
Oy		1234	TTGTAGTCTTTAATGGGATCCCTCCCATCTCTAGATGATGGCCGTCAAAGACAGTGTG	1293
Dd		12604	TTGTAGTCTTTAATGGGATCCCTCCCATCTCTAGATGATGGCCGTCAAAGACAGTGTG	12663
Oy		1294	TTGAATCACCTGGAAGTGGCAATPATTAATTTTTCCAGTACAGAAATGCTGTGTGCC	1353
Dd		12664	TTGAATCACCTGGAAGTGGCAATPATTAATTTTTCCAGTACAGAAATGCTGTGTGCC	12723
Oy		1354	CATGAAGACAATAGGTTTAAAGATTTTNAGAGTTTCATTAGCTCATTTCAAGTTCCT	1413
Dd		12724	CATGAAGACAATAGGTTTAAAGATTTTNAGAGTTTCATTAGCTCATTTCAAGTTCCT	12782
Oy		1414	CTGTTTGAAGCATGCTCTCTTAGGTTTGGACTGAACCTAGACCTTTAGTCTTTTCATC	1473
Dd		12783	CTGTTTGAAGCATGCTCTCTTAGGTTTGGACTGAACCTAGACCTTTAGTCTTTTCATC	12842
Oy		1474	CCAATTGACATATGATPAATTAATTCGTGGCAACACCAGCTCCAAAGACAAACTCTC	1533
Dd		12843	CCAATTGACATATGATPAATTAATTCGTGGCAACACCAGCTCCAAAGACAAACTCTC	12902
Oy		1534	CTTCGCTAACAGGTTAAGATGTCCATTCATCTCATGCCCTGATPAAAACTGATPAGGG	1593
Dd		12903	CTTCGCTAACAGGTTAAGATGTCCATTCATCTCATGCCCTGATPAAAACTGATPAGGG	12962
Oy		1594	AGAGAAATGTTAAAAATTTTCTAGGGTATCATAACTCTGTATGGAAGTCATCTGTCTTG	1653
Dd		12963	AGAGAAATGTTAAAAATTTTCTAGGGTATCATAACTCTGTATGGAAGTCATCTGTCTTG	13022
Oy		1654 A 1654		
Dd		13023 A 13023		
 RESULT 5 AAF88583				
ID	AAF88583	standard; cDNA; 1336 BP.		
XX	AAF88583;			
AC				
XX				
DT	19-NOV-2002	(first entry)		
XX				
DE	Human GCRC-4	cDNA INCYTE ID 90012430CD1 SEQ ID 52.		
XX				
KM	GCRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;			
KM	cytotoxic; neuroprotective; antiparkinsonian; hepatotropic; laxative;			
KM	cerebroprotective; antiinflammatory; vinorelbine; antibacterial; fungicide;			
KM	protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;			
KM	Parkinson's disease; Crohn's disease; constipation; infection;			
KM	gene therapy; gene; ss.			
OS	Homo sapiens.			
XX				
PN	WO200263004-A2.			
XX				
PD	15-AUG-2002.			
XX				
PF	06-FEB-2002; 2002WO-US003635.			
XX				
PR	07-FEB-2001; 2001US-0267322P.			
PR	23-FEB-2001; 2001US-0271215P.			
PR	08-MAR-2001; 2001US-0274551P.			
PR	23-MAR-2001; 2001US-0278507P.			
PR	30-MAR-2001; 2001US-0280507P.			
PR	02-APR-2001; 2001US-0281107P.			
PR	06-APR-2001; 2001US-0282121P.			
XX				
PA	(INCY-) INCYTE GENOMICS INC.			

XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG, Hafalia AUA,
 PI Kallik D, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Lu DAM,
 PI Rankum J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM,
 PI Granul RC, Khan PA, Walsh RT, Ison CH, Richardson TW, Griffin JA,
 PI Warren BA, Yang J, Lee EA, Harland L;
 XX WPI: 2002-627557/67.
 DR P-PSDB; AAB71325.
 DR
 PT New human G-protein coupled receptors (GPRC), useful for diagnosing or
 PT treating a disease or condition associated with decreased expression or
 PT over expression of functional GPRCs e.g. cancer, Alzheimer's and
 PT Parkinson's.
 XX
 PS Claim 113; Page 212-213; 23pp; English.
 XX
 CC This invention describes novel polypeptides which have anti-HIV,
 CC antiarteriosclerotic, cyostatic, neuroprotective, antiparkinsonian,
 CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
 CC antibacterial, fungicide and protozoicidal activity. The products of the
 CC invention are useful for treating a disease or condition associated with
 CC decreased expression or over expression of functional G-protein coupled
 CC receptors (GPRC), while antibodies generated against the polypeptide of
 CC the invention are useful for diagnosing a condition or disease associated
 CC with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,
 CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, cancer,
 CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
 CC The compounds described in the invention can be used for gene therapy.
 CC AAF88580-AAF88627 encode the GPRC proteins represented by AAB71322-
 CC AAB71369, described in the disclosure of the invention
 XX
 SQ Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;
 Query Match 73.0%; Score 1228.6; DB 6; Length 1336;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1242; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 569 GCGTGCAGTGTCTGGCAGATGAGAGCTGTGATTTGCAATTTGGTACCCCTGTGTCTC 628
 DB 617 GGCTGCCAGTCTCTGGCAGATGAGAGCTGTGATTTGCAATTTGGTACCCCTGTGTCTC 676
 QY 629 CCGGTATGGAATTCATGAGGAATATCAATGAGGACCTGTTTAAATTTCAAAAGACT 688
 DB 677 CCGGTATGGAATTCATGAGGAATATCAATGAGGACCTGTTTAAATTTCAAAAGACT 736
 QY 689 TGCCTTACATATGTGAAAAATCATCACTATATATGTATTTTGTTCATAGCCGTTC 748
 DB 737 TGCCTTACATATGTGAAAAATCATCACTATATATGTATTTTGTTCATAGCCGTTC 796
 QY 749 TGTGATTTCTGTGATTTCCAGGCTTATCATATATGTGATTTGATGAGGAGTACGCCA 808
 DB 797 TGTGATTTCTGTGATTTCCAGGCTTATCATATATGTGATTTGATGAGGAGTACGCCA 856
 QY 809 CTCTTTACTATCCACAGGAGTCTGAGGCTCAGCTGAAAAAATTTTATATAGGAGT 868
 DB 857 CTCTTTACTATCCACAGGAGTCTGAGGCTCAGCTGAAAAAATTTTATATAGGAGT 916
 QY 869 CATCTTGTGTTTCTTCTCCCTACAGGCTTTTATGATCTTATTAATTTGATGAC 928
 DB 917 CATCTTGTGTTTCTTCTCCCTACAGGCTTTTATGATCTTATTAATTTGATGAC 976
 QY 929 GCATTTCAATGCTGTGAGCAGAGGTTGATTTTATATAGGAATCTTTGAGTGTAC 988
 DB 977 GCATTTCAATGCTGTGAGCAGAGGTTGATTTTATATAGGAATCTTTGAGTGTAC 1036
 QY 989 AGCAATTAAGCTGTATGATTTGCTCTTTGTTGTTGGGGAAGCAATTTGTTAAGA 1048
 DB 1037 AGCAATTAAGCTGTATGATTTGCTCTTTGTTGTTGGGGAAGCAATTTGTTAAGA 1096
 QY 1049 AAAGATATGCTGTATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1108
 DB 1097 AAAGATATGCTGTATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1156
 QY 1109 ATTGCTTCTTATATTTGGAAT-AAAGATGATTTGAGGAGTATGATTTGTTCA 1167
 DB 1157 ATTGCTTCTTATATTTGGAAT-AAAGATGATTTGAGGAGTATGATTTGTTCA 1216
 QY 1168 TTACTGATCAAAACATGCTGTATGATTTGATGATTTGATGATTTGATGATTTGAT 1227
 DB 1217 TTACTGATCAAAACATGCTGTATGATTTGATGATTTGATGATTTGATGATTTGAT 1276
 QY 1228 CCTCATTTGATGCTTTATGGAATCCTCCATCTGAGTGTATGCT 1274
 DB 1277 CCTCATTTGATGCTTTATGGAATCCTCCATCTGAGTGTATGCT 1323

RESULT 6
 AAF88584
 ID AAF88584 standard; cDNA; 1340 BP.
 XX
 AC AAF88584;
 XX
 DT 19-NOV-2002 (first entry)
 XX
 DE Human GPRC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.
 XX
 KW GPRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
 KW cyostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
 KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
 KW protozoicidal; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
 KW Parkinson's disease; Crohn's disease; constipation; infection;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200263004-A2.
 XX
 PD 15-AUG-2002.
 XX

	FE	06-FEB-2002; 2002WO-USO03635.	
XX	PR	07-FEB-2001; 2001US-0267322P.	
XX	PR	23-FEB-2001; 2001US-027121SP.	
PR	08-MAR-2001; 2001US-0274551P.		
PR	23-MAR-2001; 2001US-0278507P.		
PR	30-MAR-2001; 2001US-0280597P.		
PR	02-APR-2001; 2001US-0281107P.		
PR	06-APR-2001; 2001US-0282121P.		
XX	(INCY-) INCYTE GENOMICS INC.		
PA	XX		
PI	Baligh MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;		
PI	Kallach DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;		
PI	Rakumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM,		
PI	Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;		
PI	Warren BA, Yang J, Lee EA, Harland L;		
XX	WPI: 2002-627557/67.		
DR	P-PDSB: AAB71326.		
XX			
PS	Claim 114, Page 213; 23pp; English.		
XX	This invention describes novel polypeptides which have anti-HIV,		
CC	antiartherosclerotic, cytostatic, neuroprotective, antiparkinsonian,		
CC	hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,		
CC	antibacterial, fungicide and protozoacide activity. The products of the		
CC	invention are useful for treating a disease or condition associated with		
CC	decreased expression or over expression of functional G-protein coupled		
CC	receptors (GPCRs), while antibodies generated against the polypeptide of		
CC	the invention are useful for diagnosing a condition or disease associated		
CC	with the expression of GPCR e.g. arteriosclerosis, cirrhosis, cancer,		
CC	stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,		
CC	constipation, AIDS, or bacterial, viral, fungal or protozoan infections.		
CC	The compounds described in the invention can be used for gene therapy.		
CC	AATF8580-AAF8627 encode the GPCR proteins represented by AAB71322-		
CC	AAB71369, described in the disclosure of the invention		
XX	SQ Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;		
	Query Match 65.7%; Score 1106.2; DB 6; Length 1340;		
	Best Local Similarity 99.6%; Pred. No. 0;		
	Matches 1119; Conservativity 0; Mismatches 3; Indels 1; Gaps 14;		
OY	153 AAATGAGCTTCCCAGAATAGCGGGACCAAAATCCTGCAGGAATTTCCTTGCGATCT	212	
Dd	205 ACAAGTAGCTTCCCAAGTAATGTCTTGGCCAACAATACCCTCAAGGAATTTCTTTGCCATCT	264	
OY	213 ATAGTGAACCCCATTAATAGACTCTTAATCATAGTCTTATTGAGCGGCTGTGGGT	272	
Dd	265 ATAAGAACACCCCACTTAATCAGGCTTAATCAATGATTAATGATGAGGCTGTGGGT	324	
OY	273 GTCAATTCATTTCTTTCTCTCTCGTGAATAATGAACACCCGTCAGTGAACCAATGGC	332	
Dd	325 GTCAATTTTCATTTCTTTCTCTCTGTGAATAATGAACACCCGTCAGTGAACCAATGGC	384	
OY	333 GTCAATTAATCTGGNGTGTGTGCACAGCGTTTTTCGTCGACAGNAGCATTTGCTTGAAC	392	
Dd	385 GTCAATTAATCTGGNGTGTGTGCACAGCGTTTTTCGTCGACAGNAGCATTTGCTTGAAC	444	
OY	393 TAACCTATCAAAGAAGACTTGAATGTTTGGGCTGCCCTTCGAAAATTTGTGAGTGCATG	452	
Dd	445 TAACCTATCAAAGAAGACTTGAATGTTTGGGCTGCCCTTCGAAAATTTGTGAGTGCATG	504	
OY	453 CTGCACATCCACATGTACTCAAGTTCTCTATTATGTGTGATCTGGTCAACGATAC	512	
Dd	505 CTGCACATCCACATGTACTCAAGTTCTCTATTATGTGTGATCTGGTCAACGATAC	564	

OY	513	CTGATCTTTCTTCAAGTCCAAAGCAAAAGTGAATTTCTACAGAAACCTGCATGCGTGGCT	572
Db	565	CTTATCTTTCTTCAAGTCCAAAGCAAAAGTGAATTTCTACAGAAACCTGCATGCGTGGCT	624
OY	573	GCCAGTCTGGCAATGTGGAAGCTGGTGAATTTGTCATTTGGTGAACCCCTGGTGTGCTCCGG	632
Db	625	GCCAGTCTGGCAATGTGGAAGCTGGTGAATTTGTCATTTGGTGAACCCCTGGTGTGCTCCGG	684
OY	633	TATGGAATCCATGAGGAATACATGAGAGACACTGTTTAAATTTCAAAAGACTTGCT	692
Db	685	TATGGAATCCATGAGGAATACATGAGAGACACTGTTTAAATTTCAAAAGACTTGCT	744
OY	693	TACGACATGAGAAAATCAATCAACTATATATATGTCAATTTTGTCAATAGCCGTGTGCTG	752
Db	745	TACGACATGAGAAAATCAATCAACTATATATATGTCAATTTTGTCAATAGCCGTGTGCTG	804
OY	753	ATTCTGTGGCTTCCAGAGTCTTTCATCATTTATGTGATGGTGCAGAAAGTACGCCACTCT	812
Db	805	ATTCTGTGGCTTCCAGAGTCTTTCATCATTTATGTGATGGTGCAGAAAGTACGCCACTCT	864
OY	813	TTACTATCCACACAGAGTTCTGGGCTCAGCTGAAAACTATTTTATATAGGGGTCATC	872
Db	865	TTACTATCCACACAGAGTTCTGGGCTCAGCTGAAAACTATTTTATATAGGGGTCATC	924
OY	873	CTTGTTGTTGTTCCCTCCCTACAGTCTTTTAGATCTATTACTTGAATGTTTGACGCAT	932
Db	925	CTTGTTGTTGTTCCCTCCCTACAGTCTTTTAGATCTATTACTTGAATGTTTGACGCAT	984
OY	933	TCCAAATGCTGTAGCAGACAGAGTTGCAATTTTATACGAAATCTTCTGAGTGTAAACAGCA	992
Db	985	TCCAAATGCTGTAGCAGACAGAGTTGCAATTTTATACGAAATCTTCTGAGTGTAAACAGCA	1044
OY	993	ATTAGCTGCTATGATTTGCTCTCTTTGTCTTTGGGGAAAGCCATTTGGTTAAAGCAAAAG	1052
Db	1045	ATTAGCTGCTATGATTTGCTCTCTTTGTCTTTGGGGAAAGCCATTTGGTTAAAGCAAAAG	1104
OY	1053	ATAATTTGGCTTATGGAATTTGTGTTTGTGGCCGTAGCCACAAACTACAGTATTCATATTT	1112
Db	1105	ATAATTTGGCTTATGGAATTTGTGTTTGTGGCCGTAGCCACAAACTACAGTATTCATATTT	1164
OY	1113	GCTTCCTTTATATGGGAAT-AAATAGGGATATAGGGAGGTAAAGATGATTTCAATAC	1171
Db	1165	GCTTCCTTTATATGGGAATTTAAATAGGGATATAGGGAGGTAAAGATGATTTCAATAC	1224
OY	1172	TTGATCAAAAACCATGCTTGATGTATGCCAAACAAAGAGCTATTAATATGCAAGAGCCT	1231
Db	1225	TTGATCAAAAACCATGCTTGATGTATGCCAAACAAAGAGCTATTAATATGCAAGAGCCT	1284
OY	1232	CATTGATGCTCTTATGGAATCCTCCCATCTCTGAGTGAATGC	1274
Db	1285	CATTGATGCTCTTATGGAATCCTCCCATCTCTGAGTGAATGC	1327
RESULT 7			
ID	AAf8585	standard; cDNA; 1460 BP.	
XX	AAf8585;		
XX	19-NOV-2002	(first entry)	
DE	Human GCRC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.		
KM	GCRC; Human; G-protein coupled receptor; anti-HIV; antiaretrosclerotic;		
KM	cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;		
KM	cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;		
KM	protozoacide; clirhosis; cancer; stroke; Alzheimer's disease; AIDS;		
KM	Parkinson's disease; Crohn's disease; constipation; infection;		
XX	gene therapy; gene; ss.		
OS	Homo sapiens.		
PN	WO200263004-A2.		

XX 15-AUG-2002.
PD
XX 06-FEB-2002; 2002WO-US003635.
PF
XX 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX
XX (INCYTE GENOMICS INC.
PA
XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yeo MG, Haffalia AUA,
PI Kallik DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Lu DAM;
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Griffin JA,
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffen JA,
PI Warren BA, Yang J, Lee EA, Harland L;
XX WPI, 2002-627557/67.
DR P-PSDB; AAB71327.
XX
XX New human G-protein coupled receptors (GPRC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT overexpression of functional GPRCs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX
XX Claim 15; Page 213-214; 239pp; English.
XX
CC This invention describes novel polypeptides which have anti-HIV,
CC antiaerotoxic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatocytic, laxative, cerebroprotective, antiinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or overexpression of functional G-protein coupled
CC receptors (GPRC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GPRC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAB71369, described in the disclosure of the invention
CC
CC AAB71369, described in the disclosure of the invention
CC
SQ Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;

Query Match 65.7%; Score 1106.2; DB 6; Length 1460;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 153 AAATGTGACTTCCCAAGTATGCTGCGCAGATACCTCAGGAATTCCTTGGCATCT 212
DB 335 ACAGGTGACTTCCCAAGTATGCTGCGCAGATACCTCAGGAATTCCTTGGCATCT 384

QY 213 ATAGTACACCCCACTTATACAGCTTATCATAGTCTTATTTGGCGGCTGTGGGT 272
DB 385 ATAGTACACCCCACTTATACAGCTTATCATAGTCTTATTTGGCGGCTGTGGGT 444

QY 273 GTGATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTGACCACTTGGCG 332
DB 445 GTGATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTGACCACTTGGCG 504

QY 333 GTGATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTTGGCGTGAAC 392
DB 505 GTGATTTTCATTTCTTTCTCTGCTGTAATAAGAACCCGGTCACTTGGCGTGAAC 564

QY 393 TACCTCATCAG 452
DB 565 TACCTCATCAG 624

QY 453 CTGACATCCACATGATCTACAGTTCTTCTATTTGAGTGTCTGTGTGACCAAGATAC 512

DB 625 CTGACATCCACATGATCTACAGTTCTTCTATTTGAGTGTCTGTGTGACCAAGATAC 684
QY 513 CTGATCTTCTTCAAGTGCAG 572
DB 685 CTGATCTTCTTCAAGTGCAG 744
QY 573 GCGAGTGTGAG 632
DB 745 GCGAGTGTGAG 804
QY 633 TATGAGATCCATGAG 692
DB 805 TATGAGATCCATGAG 864
QY 693 TACACATATGAG 752
DB 865 TACACATATGAG 924
QY 753 ATTCTGTTGCTTCTTCCAGGCTTCTATCTTATTTGATGAGAGAGAGAGAGAGAGAG 812
DB 925 ATTCTGTTGCTTCTTCCAGGCTTCTATCTTATTTGATGAGAGAGAGAGAGAGAGAG 984
QY 813 TTACTATCCACAG 872
DB 985 TTACTATCCACAG 1044
QY 873 CTGTTGTTGCTTCTTCCAGGCTTCTATCTTATTTGATGAGAGAGAGAGAGAGAGAG 932
DB 1045 CTGTTGTTGCTTCTTCCAGGCTTCTATCTTATTTGATGAGAGAGAGAGAGAGAGAG 1104
QY 933 TCACATGCTGAG 992
DB 1105 TCACATGCTGAG 1164
QY 993 ATTGAGTGTGAG 1052
DB 1165 ATTGAGTGTGAG 1224
QY 1053 ATAAATGCTTATGAG 1112
DB 1225 ATAAATGCTTATGAG 1284
QY 1113 GCTTCTTATATGAG 1171
DB 1285 GCTTCTTATATGAG 1344
QY 1172 TTGATCCAAACAG 1231
DB 1345 TTGATCCAAACAG 1404
QY 1232 CATTGATGCTTATGAG 1274
DB 1405 CATTGATGCTTATGAG 1447

RESULT 8
AAB37670
ID AAB37670 standard; cDNA; 1499 BP.
XX
XX AAB37670;
XX
DE 27-AUG-2002 (first entry)
XX
XX Human G-protein coupled receptor-6 (GPRC-6) cDNA.
XX
XX Human, G-protein coupled receptor-6; GPRC-6; atherosclerosis; cancer;
XX cell proliferative disorder; gastrointestinal; autoimmune; metabolic;
XX neurological; inflammatory; cardiovascular; viral infection; anorexia;
XX cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;
XX Alzheimer's disease; heart failure; hepatitis; cholelithiasis; obesity;
XX rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;
XX osteoporosis; gene; 88.

```
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT Key 381..1400
XX FT CDS /*tag=a
XX FT /product="Human GCRC-6 protein"
XX PN
XX PD
XX PD 04-APR-2002.
XX PF
XX PF 28-SEP-2001; 2001WO-US030661.
XX PR
XX PR 29-SEP-2000; 2000US-0236546P.
XX PR 13-OCT-2000; 2000US-0240589P.
XX PR 20-OCT-2000; 2000US-0242223P.
XX PR 20-OCT-2000; 2000US-0242322P.
XX PR 03-NOV-2000; 2000US-0245855P.
XX PR 03-NOV-2000; 2000US-0245900P.
XX PR 09-NOV-2000; 2000US-0247587P.
XX PR 15-NOV-2000; 2000US-0249343P.
XX PA
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Baughn MR, Graul RC, Walia NK, Gandhi AR, Hafalia AD;
XX PI Rankumar J, Tribouley CM, Thornton M, Kalliock DA, Yao MG;
XX PI Elliott VS, Buford N, Khan FA, Yue H, Lu Y, Arizun C, Roopa R;
XX PI Nguyen DB, Lee EA, Lu DM, Ison CH, Walsh RT, Policky JL;
XX DR WPI; 2002-426012/45.
XX DR P-PSDB; AAE23414.
XX PT
XX PT Novel G-protein coupled receptor polypeptides referred as GCRC peptides,
XX PT useful for treating multiple sclerosis, cholecystitis heart failure,
XX PT angina pectoris, rheumatoid arthritis, obesity, osteoporosis.
XX PS
XX PS Claim 83; Page 140; 147pp; English.
XX CC
XX CC The invention relates to human G-protein coupled receptor (GCRC 1-16)
XX CC polypeptides and polynucleotides. Sequences of the invention are useful
XX CC for the diagnosis, treatment and prevention of cell proliferative (e.g.
XX CC cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's
XX CC disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,
XX CC heart failure), gastrointestinal (e.g. anorexia, cholecystitis),
XX CC autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)
XX CC and metabolic disorders (e.g. obesity, osteoporosis), viral infections,
XX CC atherosclerosis and hepatitis. GCRC proteins are useful for identifying
XX CC compounds that modulate, mimic and block olfactory and taste sensations.
XX CC They are also useful for identifying GCRC modulators. GCRC DNAs are
XX CC useful in gene therapy. The present sequence is human GCRC-6 cDNA
XX SQ
XX SQ Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;
XX
XX Query Match 61.2%; Score 1030; DB 6; Length 1499;
XX Best Local Similarity 98.6%; Pred. No. 1.3e-292;
XX Matches 1091; Conservative 0; Mismatches 10; Indels 5; Gaps 5;
XX
XX 157 GTGACTTCCCAAGATGCTGGCCACCAATACCTCCAGGAATTCCTCTTGCACTCTATAG 216
XX DB GTGACTTCCCAAGATGCTGGCCACCAATACCTCCAGGAATTCCTCTTGCACTCTATAG 426
XX
XX 217 TGAACCCCACTTATACGCTCTACTTATAGTGTATAGGCGGCTGGTGGGTGCA 276
XX DB TGAACCCCACTTATACGCTCTACTTATAGTGTATAGGCGGCTGGTGGGTGCA 486
XX
XX 277 TTTCATTCTTTCTCTCTGTGAAATGAACACCCGGTCAGTGACCAACATGGCGGTCA 336
XX DB TTTCATTCTTTCTCTCTGTGAAATGAACACCCGGTCAGTGACCAACATGGCGGTCA 546
XX
XX 487 TTTCATTCTTTCTCTCTGTGAAATGAACACCCGGTCAGTGACCAACATGGCGGTCA 546
XX
XX 337 TTAACCTGCTGTGCTGACAGCGTTTCTGCTGACAGTCCATTTGCTGACCTTACC 396
XX DB TTAACCTGCTGTGCTGACAGCGTTTCTGCTGACAGTCCATTTGCTGACCTTACC 606
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QY 397 TCATCAAGAGAAGCTTGAGTGTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCATGCTGC 456
DB TCATCAAGAGAAGCTTGAGTGTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCATGCTGC 666
QY 457 ACATCCACATGATCCTGACGCTTCTATTTCTATGTGTGATCTGTGACCAAGATACCTCA 516
DB ACATCCACATGATCCTGACGCTTCTATTTCTATGTGTGATCTGTGACCAAGATACCTCA 726
QY 517 TCTTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGCTGCCA 576
DB TCTTCTTCAAGTGCAGAAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGCTGCCA 786
QY 577 GTGCTGACATGTGAGCGCTGTGATTTGTCAATGATGATGATGATGATGATGATGATGATGATG 636
DB GTGCTGACATGTGAGCGCTGTGATTTGTCAATGATGATGATGATGATGATGATGATGATGATG 846
QY 637 GAATCCATGAGGAATACATGAGAGACATGTTTAAATTTCAAAAAGACCTTGCTTACA 696
DB GAATCCATGAGGAATACATGAGAGACATGTTTAAATTTTCAAAAAGACCTTGCTTACA 906
QY 697 CATATGTGAAATCATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATG 756
DB CATATGTGAAATCATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATG 966
QY 757 TGTGATCTTCCAGATCTTCATCATATATGTTGATGATGATGATGATGATGATGATGATGATG 816
DB TGTGATCTTCCAGATCTTCATCATATATGTTGATGATGATGATGATGATGATGATGATGATG 1026
QY 967 TGTGATCTTCCAGATCTTCATCATATATGTTGATGATGATGATGATGATGATGATGATGATG 1026
DB TATCCACACAGAGATCTGAGGCTCAGCTGAAAAACCTATTTTATATGAGGATCATCTTG 1086
QY 817 TATCCACACAGAGATCTGAGGCTCAGCTGAAAAACCTATTTTATATGAGGATCATCTTG 876
DB TATCCACACAGAGATCTGAGGCTCAGCTGAAAAACCTATTTTATATGAGGATCATCTTG 1086
QY 877 TTTGTTTCTTCCCTACCACTTCTTATGATATCTATATCTGATGATGATGATGATGATGATGATG 936
DB TTTGTTTCTTCCCTACCACTTCTTATGATATCTTATATCTGATGATGATGATGATGATGATG 1146
QY 1087 TTTGTTTCTTCCCTACCACTTCTTATGATATCTTATATCTGATGATGATGATGATGATGATG 1146
DB ATGCTGTACAGCAAGTGTGATTTATATACGAATCTCTTGAAGTAAACAGCAATTA 996
QY 1147 ATGCTGTACAGCAAGTGTGATTTATATACGAATCTCTTGAAGTAAACAGCAATTA 1206
QY 997 GCTGTATATGATTTGCTTCTTTGCTTTGAGGAGAACCATGAGTTTAAACAAAGATTA 1056
DB GCTGTATATGATTTGCTTCTTTGCTTTGAGGAGAACCATGAGTTTAAACAAAGATTA 1266
QY 1207 GCTGTATATGATTTGCTTCTTTGCTTTGAGGAGAACCATGAGTTTAAACAAAGATTA 1266
DB TTGGCTTATGGAATTTGTTTGTGCGGTAGCCACAACTACAGTATTCATATTTGCTT 1324
QY 1057 TTGGCTTATGGAATTTGTTTGTGCGGTAGCCACAACTACAGTATTCATATTTGCTT 1116
DB TTGGCTTATGGAATTTGTTTGTGCGGTAGCCACAACTACAGTATTCATATTTGCTT 1324
QY 1117 CTTTATATGAGGAAT-AAATGAGTATAGGAGATGATGATGATGATGATGATGATGATGATGATG 1175
DB CTTTATATGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1384
QY 1325 CTTTATATGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1384
DB TCAAAACATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1235
QY 1176 TCAAAACATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1235
DB TC-AAAGCATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1442
QY 1385 TC-AAAGCATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1442
DB GTAGTCTTATGGAATCCCTCCATC 1261
QY 1236 GTAGTCTTATGGAATCCCTCCATC 1261
DB GTAGTCTTATGGAATCCCTCCATC 1468
XX
XX RESULT 9
XX ABR87351
XX ID ABR87351 standard; cDNA; 1051 BP.
XX
XX AC ABR87351;
XX
XX DT 24-SEP-2002 (first entry)
XX
XX DE Human cDNA encoding G protein-coupled receptor IGS70.
XX
XX KW Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS;
```

psychiatric disorder; central nervous system disorder; schizophrenia;
 Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
 heart failure; angina pectoris; myocardial infarction; kidney disease;
 renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
 inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
 asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
 osteoporosis; allergy.

Homo sapiens.

Key Location/Qualifiers
 CDS 60..977
 FT /*tag= a
 FT /product= "GPCR IGS70"

MO200244212-A2.

06-JUN-2002.

23-NOV-2001; 2001MO-EP013706.

30-NOV-2000; 2000EP-00204280.
 05-DEC-2000; 2000US-0251045P.

(SOLV) SOLVAY PHARM BV.

Deleersnyder W, Blockx H, De Moor L;
 WPI; 2002-527703/56.
 P-PSDB; AAU99179.

Novel G-protein coupled receptor IGS70 polypeptide useful for treating
 dysfunctions, disorders or disease related to lung, bone marrow, spinal
 cord immune system.

Claim 1; Page 6; 58pp; English.

The invention relates to a G protein-coupled receptor (GPCR) IGS70
 polypeptide including sequences that are 98-99.6% identical. Also
 included are the polynucleotide encoding IGS70 (including sequences 98-
 99.6% identical to the polynucleotide or the DNA insert contained in
 plasmid CBS 109818), a hybridisation probe derived from the
 polynucleotide, a DNA or RNA expression system producing IGS70, a host
 comprising the expression system, IGS70 receptor membrane preparation
 derived from the cell, an antibody immunospecific for IGS70, IGS70 is
 useful for diagnosing a disease or a susceptibility to disease in a
 subject related to expression or activity of the IGS70 polypeptide in a
 subject by determining the presence or absence of mutation in the
 nucleotide sequence encoding IGS70 in the genome of the subject in a
 sample derived from the subject. IGS70 is also useful identifying agonist
 or antagonist. The IGS70 protein, polynucleotide, antibody and identified
 ant/agonists are useful for treating psychiatric and central nervous
 system (CNS) disorders such as schizophrenia, Alzheimer's disease,
 multiple sclerosis, anxiety, cardiovascular diseases such as heart
 failure, angina pectoris, myocardial infarction, kidney disease such as
 renal failure, gastrointestinal disorders such as irritable bowel
 syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
 inflammation, cancers, asthma, infection (such as bacterial, viral,
 fungal, protozoal) especially human immunodeficiency virus infection
 (HIV), diabetes, osteoporosis and allergies. The present sequence encodes
 the human GPCR IGS70

Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 58.9%; Score 991.2; DB 6; Length 1051;
 Best Local Similarity 99.6%; Pred. No. 3.1e-281;
 Matches 1004; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

155 ATGTGACTTCCAGATATGCTGGCCAAATACCTCCAGAAATCTCTTCCGATCTTAT 214
 DB 44 AGGTGACTTCCAGATATGCTGGCCAAATACCTCCAGAAATCTCTTCCGATCTTAT 103
 215 AGTGACACCCCACTTAATCAAGCTCTTACTTATGTGCTTATGCGGGCTGGTGGGT 274

DB 104 AGTGACACCCCACTTAATCAAGCTCTTACTTATGTGCTTATGCGGGCTGGTGGGT 163
 QY 215 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 334
 DB 164 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 223
 QY 335 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 394
 DB 224 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 283
 QY 395 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 454
 DB 284 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 343
 QY 455 GCAATCCACATGTACCTCAGCTTCTTATCTATGTGATGCTGCTGCTGCTGCTGCTGCT 514
 DB 344 GCAATCCACATGTACCTCAGCTTCTTATCTATGTGATGCTGCTGCTGCTGCTGCTGCT 403
 QY 515 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 574
 DB 404 CATTTCATTTTCTTCTCTCTGTAAGAAATGAACACCCGTCAGTACACCATAGCGGT 463
 QY 575 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
 DB 464 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
 QY 635 TGAATTCATGAGGAAATGAGAGACCTGCTTAAATTTGACAAAGAGCTGCTGCTGCTGCT 694
 DB 524 TGAATTCATGAGGAAATGAGAGACCTGCTTAAATTTGACAAAGAGCTGCTGCTGCTGCT 583
 QY 695 CACATATGTAAGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 754
 DB 584 CACATATGTAAGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 643
 QY 755 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814
 DB 644 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
 QY 815 ACTATCCACAGGAGTTCGAGCTGAGCTGAGAAACCTATTTTATAGGGGTCATCTCT 874
 DB 704 ACTATCCACAGGAGTTCGAGCTGAGCTGAGAAACCTATTTTATAGGGGTCATCTCT 763
 QY 875 TGTGTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 934
 DB 764 TGTGTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 823
 QY 935 CAATGCTGTAAGACAGGAGTTCATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 994
 DB 824 CAATGCTGTAAGACAGGAGTTCATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 883
 QY 995 TAGTGTGTAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1054
 DB 884 TAGTGTGTAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 943
 QY 1055 AATTGCTTATGGAATTTGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1114
 DB 944 AATTGCTTATGGAATTTGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1003
 QY 1115 TTCTTATATTTGGAAT-AAATGGGTATGAGGGAGGTAAAGATGT 1161
 DB 1004 TTCTTATATTTGGAATTTGAGTATGAGGGAGGTAAAGATGT 1051

RESULT 10
 AAL57070 standard; DNA; 1040 BP.
 XX AAL57070;
 XX AC
 XX DT 17-SEP-2003 (first entry)
 XX Human G-protein coupled receptor GAVE18 DNA sequence.

XX Human G-protein coupled receptor; GAVE18; signal transduction;
KW inflammation; physiological immunological response; antiinflammatory;
KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;
KW chromosomal mapping; tissue typing; forensic biology;
KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
KW rheumatoid arthritis; gene; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "GAVE18 protein"
XX
EN WO2003042399-A2.
XX
PD 22-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US035887.
XX
PR 13-NOV-2001; 2001US-0354150P.
PR 22-MAR-2002; 2002GB-00006891.
XX
PA (AVET) AVENTIS PHARM INC.
XX
PI Eisingdrelo H, Cai J, Busch SJ, Gassenhuber J;
XX
DR WPI; 2003-457496/43.
DR P-PSDB; AAO27265.
XX
PT New GAVE18 polypeptide and nucleic acid molecule encoding the
PT polypeptide, useful for preventing and treating a disease or disorder
PT associated with aberrant expression or activity of GAVE18, e.g. asthma or
PT rheumatoid arthritis.
XX
PS Claim 1; Fig 5; 88pp; English.
XX
CC This invention relates to a novel G-protein coupled receptor (GAVE18)
CC that is involved in signal transduction in respect to inflammation and
CC the physiological immunological response. Molecules which may modulate
CC the signalling activity or signal transduction of the receptor may be
CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The
CC GAVE18 receptor and the DNA sequence encoding it may be a target for
CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18
CC proteins and antibodies may be useful in screening assays, detection
CC assays (for example chromosomal mapping, tissue typing or forensic
CC biology), or predictive medicine (for example diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics. The
CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse
CC agonist and antagonist are also useful for preventing and treating a
CC disease or disorder associated with aberrant expression or activity of
CC GAVE18, such as inflammation and immunological-related diseases or
CC disorders, for example asthma, chronic obstructive pulmonary disease or
CC rheumatoid arthritis. The present sequence is the DNA sequence encoding
CC the GAVE18 protein of the invention
XX
SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;
Query Match 57.5%; Score 968; DB 9; Length 1040;
Best Local Similarity 99.4%; Pred. No. 2,1e-274;
Matches 982; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 171 ATGCTGGCCACATATCTCCAGAAATTCCTCTTGCAATCTCTATATGACACCCCACTTA 230
DB 1 ATGCTGGCCACATATCTCCAGAAATTCCTCTTGCAATCTCTATATGACACCCCACTTA 60
QY 231 ATCAGCCCTCTATCTTATGATGCTTATGCGGCGCGGCGGAGTCAATTCATCTTTTC 290
DB 61 ATCAGCCCTCTATCTTATGATGCTTATGCGGCGCGGCGGAGTCAATTCATCTTTTC 120
QY 291 CTCCTGTGAAATGACACCCCGGTCACTGACCAACCATGCGGCTCATTAATCTGTGTG 350
|||||

DB 121 CTCCTGTGAAATGACACCCCGGTCACTGACCAACCATGCGGCTCATTAATCTGTGTG 180
QY 351 GTCACAGAGGTTTTTTCGTGACAGATGCAATTTGCTTGACCTACCTCATCAAGAACT 410
DB 181 GTCACAGAGGTTTTTTCGTGACAGATGCAATTTGCTTGACCTACCTCATCAAGAACT 240
QY 411 TGGATGTTTTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCATGTCACATGATGAC 470
DB 241 TGGATGTTTTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCATGTCACATGATGAC 300
QY 471 CTGACGTTCTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 530
DB 301 CTCACGTTCTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 531 AAAGACAAAGTGAATTCACAGAAAATGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
DB 361 AAAGACAAAGTGAATTCACAGAAAATGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 591 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 650
DB 421 ACGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 651 TACATGAGAGCACTGTTTTTAATTTACAAAGAGCTGCTTACACATATGTAATATC 710
DB 481 TACATGAGAGCACTGTTTTTAATTTACAAAGAGCTGCTTACACATATGTAATATC 540
QY 711 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 770
DB 541 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 771 GTCCTCATCTATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 830
DB 601 GTCCTCATCTATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 831 TTCTGGGCTGAGCTGAAAAACCTATTTTATATGAGGCTATCTTGTGTTCTTCTCC 890
DB 661 TTCTGGGCTGAGCTGAAAAACCTATTTTATATGAGGCTATCTTGTGTTCTTCTCC 720
QY 891 TACAGTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 950
DB 721 TACAGTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 951 AAGGTGCAATTTTATTAACGAATCTCTTGATGATGATGATGATGATGATGATGATG 1010
DB 781 AAGGTGCAATTTTATTAACGAATCTCTTGATGATGATGATGATGATGATGATGATG 840
QY 1011 CTCTCTCTTGTCTTTGGGGGAGACCATTTGTTTAAAGCAAAAGTAAATGCTTATG 1070
DB 841 CTCTCTCTTGTCTTTGGGGGAGACCATTTGTTTAAAGCAAAAGTAAATGCTTATG 900
QY 1071 TGGTTTTTGGCGTTAGCCAAACTACAGTATTCATTTGCTTCTTATATGAGGA 1130
DB 901 TGGTTTTTGGCGTTAGCCAAACTACAGTATTCATTTGCTTCTTATATGAGGA 960
QY 1131 AT-AAATGGGTATAGGGAGGTAGGA 1157
DB 961 ATAAATGGGTATAGGGAGGAAAAAAA 988
RESULT 11
AAL53414
ID AAL53414 standard; DNA; 939 BP.
XX
AC AAL53414;
DT 12-DEC-2002 (first entry)
XX
DE 939 nt coding DNA of a human G-protein coupled receptor type protein.
KW Anti-HIV; cyrostatic; antidiabetic; antiasthmatic; antiinflammatory;
KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
KW cardiant; dermatological; antifertility; hepatotropic; antiallergic;

KM	antipneumatic; ophthalmological; antiangular; antithyroid; anticonvulsant;
KM	antipneumatic; antichratic; G-protein coupled receptor; subfamily I;
KM	93870 receptor; immune; inflammatory disorder; platelet disorder;
KW	skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
KW	cellular proliferative; differentiative disorder; hormonal disorder;
KV	monoclonal disorder; cardiovascular disorder; viral disease; pain;
KV	liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
KM	hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
KV	viral meningitis; fungal meningoencephalitis; multiple sclerosis;
KM	Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
KV	myocardial infarction; heart failure; angina pectoris; dermatitis;
KM	myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
KM	inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
KM	conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
KW	transgenic animal; human; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	
FT	
FT	CDS
FT	Location/Qualifiers
FT	1..939
FT	/*tag= a
FT	/partial
FT	/product= "human G-protein coupled receptor type protein
FT	93870"
FT	/note= "No stop codon"
PN	
XX	
PA	WO200270657-A2.
PD	
XX	12-SEP-2002.
PX	
PF	28-FEB-2002; 2002MO-US006455.
PR	
XX	01-MAR-2001; 2001US-0272677P.
PA	(MILL-) MILLENNIUM PHARM INC.
PI	
DR	Gluckermann MA;
XX	
DR	WPI: 2002-732793/79.
XX	P-PADB; AAO22919.
PT	
PT	New G-protein coupled receptor used in receptor assays as a target for
PT	diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT	inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT	disorders.
PS	
Claim 5; Page 101-103; 105pp: English.	
XX	
XX	The invention relates to an isolated polypeptide, which is a G-protein
CC	coupled receptor (GPCR) related to subfamily I of G-protein coupled
CC	receptor type proteins (GPCRs), designated the 93870 receptor. The
CC	polypeptides, nucleic acid molecules and antibodies of the invention are
CC	useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC	monitoring clinical trials or pharmacogenetics), or in methods of
CC	treatment (e.g. therapeutic and prophylactic). They are useful in
CC	treating and diagnosing conditions related to aberrant activity or
CC	expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC	inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC	disorders, or bone marrow mononuclear disorders, as well as cellular
CC	proliferative and/or differential disorders, hormonal disorders,
CC	neurological disorders, cardiovascular disorders, viral diseases, liver
CC	disorders, and pain and metabolic disorders. Conditions that can be
CC	treated include cancer, diabetes mellitus, hypothyroidism,
CC	hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC	viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC	Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC	Huntington's disease, heart failure, angina pectoris, myocardial
CC	infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC	inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC	disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC	transgenic animals are useful for studying the function and/or activity
CC	of a 93870 protein and for identifying and/or evaluating modulators of
CC	93870 protein. The polynucleotides of the invention can be used in
CC	93870 activities.

Query Match	55.8%	Score 939	DB 6	Length 939
Beet Local Similarity	100.0%	Pred. No. 7.2e-266		
Matches	939	Conservative	0	Mismatches 0; Indels 0; Gaps 0
CC	gene therapy. This polynucleotide sequence represents the 939 nucleotide			
CC	DNA of the human G-protein coupled receptor type protein of the invention			
XX				
XX				
SQ	Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;			
QY	147	ATGCAAAATGAGCTTCCCAAGATATGCTGCGCCACATACCTCCAGAAATTCCTTGGC	206	
DB	1	ATGCAAAATGTGACTTCCCAAGTATGCTCTGCGCCACATACCTCCAGAAATTCCTTGGC	60	
QY	207	GATCCTATATGAGACACCCCACTTATATACGCTCTACTATATAGTCTTATTTGGCGGGCTG	266	
DB	61	GATCCTATATGAGACACCCCACTTATATAGCCTCTATCTTATATAGTCTTATTTGGGGGGCTG	120	
QY	267	GTGGGTGCATTTTCATTTCTTTTCTCTCTGTGTGAAATGAACACCCGGTCACTGACCAAC	326	
DB	121	GTGGGTGCATTTTCATTTCTTTTCTCTCTGTGTGAAATGAACACCCGGTCACTGACCAAC	180	
QY	327	ATGGCGGTCAATTAATCTGGTGTGTGTCCACAGCGTTTTCGTGTGACAGTGCATTTGGC	386	
DB	181	ATGGCGGTCAATTAATCTGTGTGTGTGTCCACAGCGTTTTCGTGTGACAGTGCATTTGGC	240	
QY	387	TTGACCTTACCTCATCAAGAGAACTTGTGATTTTGGGCTGCCCTTCGCAAAATTTGTGAGT	446	
DB	241	TTGACCTTACCTCATCAAGAGAACTTGTGATTTTGGGCTGCCCTTCGCAAAATTTGTGAGT	300	
QY	447	GCCATGTGCACATCCACATATATACCTCAGTTCCTTCTATATGTGTATCTCTGGTCAAC	506	
DB	301	GCCATGTGCACATCCACATATATATACCTCAGTTCCTTCTATATGTGTATCTCTGGTCAAC	360	
QY	507	AGATACCTGCATCTCTTCAAGTATGAGAAAGCAACGTGAATCTTACAGAAACTGTGATCT	566	
DB	361	AGATACCTGCATCTCTTCAAGTATGAGAAAGCAACGTGAATCTTACAGAAACTGTGATCT	420	
QY	567	GTGGCTGCAGTGTGTGCATATGTGACGCTGTGTGATTTGTATTTGTATGTCACCTGGTTC	626	
DB	421	GTGGCTGCAGTGTGTGCATATGTGACGCTGTGTGATTTGTATTTGTATGTCACCTGGTTC	480	
QY	627	TCCCGGTATGGAATCCATGAGAAATPACATGAGAGCACTGTTTTAAATTTACAAAGAG	686	
DB	481	TCCCGGTATGGAATCCATGAGAAATPACATGAGAGCACTGTTTTAAATTTACAAAGAG	540	
QY	687	CTTGTCTTACATATGTGAAATATCATCATATATATGATATGTCATTTTGTCAATAGCCGT	746	
DB	541	CTTGTCTTACATATGTGAAATATCATCATATATATGATATGTCATTTTGTCAATAGCCGT	600	
QY	747	GCTGTGATTCCTGTGTGCTTCCAGGTCTTATCATTTATATGATGTGTGACAGAGCTAGC	806	
DB	601	GCTGTGATTCCTGTGTGCTTCCAGGTCTTATCATTTATGTGTGTGTGACAGAGCTAGC	660	
QY	807	CACCTTTTACTATCCACACAGAGTCTTGCGCTCAGCTGAAAAAACCTATTTTATATAGG	866	
DB	661	CACCTTTTACTATCCACACAGAGTCTTGCGCTCAGCTGAAAAAACCTATTTTATATAGG	720	
QY	867	GTATCTCTGTGTGTCTTCTCTCTCTTACAGTCTTTATAGATCTATTAATTGAATGTGTG	926	
DB	721	GTATCTCTGTGTGTGTCTTCTCTCTCTTACAGTCTTTATAGATCTATTAATTGAATGTGTG	780	
QY	927	ACGCAATTCGAATGCTGTGAGAGAGAGGTGCATTTTATATAGAAATCTTGTATAGTGA	986	
DB	781	ACGCAATTCGAATGCTGTGAGAGAGAGGTGCATTTTATATAGAAATCTTGTATAGTGA	840	
QY	987	ACAGCAATATAGCTGTATGATTTGCTTCTCTTGTCTTTTGGGGAGACCAATGTGTTAAG	1046	
DB	841	ACAGCAATATAGCTGTATGATTTGCTTCTCTTGTCTTTTGGGGAGACCAATGTGTTAAG	900	
QY	1047	CAAAAGATTAATGGCTTATGGAATTTGTGTTTGTGCGCT	1085	
DB	901	CAAAAGATTAATGGCTTATGGAATTTGTGTTTGTGCGCT	939	

```
RESULT 12
AAL44713
ID AAL44713 standard; DNA; 918 BP.
XX
AC AAL44713;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human testis originated G-protein coupled receptor TGR10 coding sequence.
XX
KW Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
KW cytosolic; immunomodulator; cardiant; neuroprotective; gene therapy;
KW inflammation; nervous system disease; circulatory system disease; cancer;
KW metabolic disease; immunological disease; gastrointestinal disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "TGR10"
XX
XX MO200196567-A1.
XX PD 20-DEC-2001.
XX PF 14-JUN-2001; 2001WO-JP005061.
XX PR 15-JUN-2000; 2000JP-00184596.
XX PR 19-JUN-2000; 2000JP-00223887.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Moriya T, Ito T, Shintani Y, Miyajima N;
XX DR WPI; 2002-098071/13.
XX DR P-PSDB; AAM48989.
XX
XX Human testis-originated G protein-coupled receptor protein TGR10 and
XX PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.
XX PT diseases of central nervous system, inflammations and diseases of
XX PT circulatory system.
XX PS Claim 5; Page 99; 110pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of a
XX CC novel human testis-originated G protein-coupled receptor protein TGR10.
XX CC The sequences can be used in the development of drugs for the treatment
XX CC of diseases of the central nervous system, inflammations, diseases of the
XX CC circulatory system, cancer, metabolic diseases, immunological diseases,
XX CC and diseases of the gastrointestinal system. The present sequence is the
XX CC coding sequence of the invention
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Query March 54.4%; Score 916.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 3.3e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 171 ATGCTGGCCACATTAACCTCCAGGAATTCCTTGGCATCTTATAGTGACACCCCACTTA 230
DB 1 ATGCTGGCCACATTAACCTCCAGGAATTCCTTGGCATCTTATAGTGACACCCCACTTA 60
QY 231 ATGAGCCTCTATCTTATAGTCTTATTTGGCGGCTGTGGTGTCACTTTCATTTCTTTTC 290
DB 61 ATGAGCCTCTATCTTATAGTCTTATTTGGCGGCTGTGGTGTCACTTTCATTTCTTTTC 120
QY 291 CTCTGTGTGAAGAAGAACCCGGTCACTGACACCAATGGGGTCACTTAATCTTGTGTGTG 350
DB 121 CTCTGTGTGAAGAAGAACCCGGTCACTGACACCAATGGGGTCACTTAATCTTGTGTGTG 180
```

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QY 351 GTCCACAGCGTTTTTCGTGTCAGTGCATTTGCTGTGACCTACCTCAACAGAAAGACT 410
DB 181 GTCCACAGCGTTTTTCGTGTCAGTGCATTTGCTGTGACCTACCTCAACAGAAAGACT 240
QY 411 TGGATGTTGGGCTGCCCTTCTGCAAAATTTTGAGTGCCATGCTGCACATCCATGTAC 470
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTTGAGTGCCATGCTGCACATCCATGTAC 300
QY 471 CTCAAGTTCCTATTCATATGATGATCCGTGGTACACAGATACCTCAATCTTCAAGTGC 530
DB 301 CTCAAGTTCCTATTCATATGATGATCCGTGGTACACAGATACCTCAATCTTCAAGTGC 360
QY 531 AAAGACAAAGTGAATTTCTACAGAAAATGECATGCTGTGCTGCCCATGTGTCATGTGG 590
DB 361 AAAGACAAAGTGAATTTCTACAGAAAATGECATGCTGTGCTGCCCATGTGTCATGTGG 420
QY 591 ACGCTGTGATTTGTCAATGTGTGTAACCCCTGTGTGTCTCCCGTATGGAATCCATGAGAA 650
DB 421 ACGCTGTGATTTGTCAATGTGTGTAACCCCTGTGTGTCTCCCGTATGGAATCCATGAGAA 480
QY 651 TACAATGAGGAGACGTTTTTAATTTCAAAAGAGCTTGCTTACATATGGAATATC 710
DB 481 TACAATGAGGAGACGTTTTTAATTTCAAAAGAGCTTGCTTACATATGGAATATC 540
QY 711 ATCAACTATATGATATGATCAATTTTGTATAGCCGTTGCTGTGATTCGTTGCTTCCAG 770
DB 541 ATCAACTATATGATATGATCAATTTTGTATAGCCGTTGCTGTGATTCGTTGCTTCCAG 600
QY 771 GTCTTCATCATATATGTTGATGTGTGACAGAACTACGCCACTCTTACTATCCACAGAG 830
DB 601 GTCTTCATCATATATGTTGATGTGTGACAGAACTACGCCACTCTTACTATCCACAGAG 660
QY 831 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTGTTGTTCCCTCC 890
DB 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTGTTGTTCCCTCC 720
QY 891 TACCAGTTCCTTATAGATCTATTAATGTAATGTTGTGACGATTCATGCTGTAGCAGC 950
DB 721 TACCAGTTCCTTATAGATCTATTAATGTAATGTTGTGACGATTCATGCTGTAGCAGC 780
QY 951 AAGGTTCATTTTATATACGAATCTTGTGAGTGAACAGCAATTTAGCTGCTATGATTTG 1010
DB 781 AAGGTTCATTTTATATACGAATCTTGTGAGTGAACAGCAATTTAGCTGCTATGATTTG 840
QY 1011 CTCTCTTTGTCTTTGGGGGAGACCATTTGGTTTAAAGAAAGATTAATTTGCTTATGGAAT 1070
DB 841 CTCTCTTTGTCTTTGGGGGAGACCATTTGGTTTAAAGAAAGATTAATTTGCTTATGGAAT 900
QY 1071 TGTGTTTGTGCGCTTAG 1088
DB 901 TGTGTTTGTGCGCTTAG 918
RESULT 13
ABA00160
ID ABA00160 standard; cDNA; 918 BP.
XX
AC ABA00160;
XX
DT 15-NOV-2002 (first entry)
XX
DE PFI-021 cDNA.
XX
KW Gene; human; G-protein coupled receptor; GPCR; PFI-021;
KW peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;
KW respiratory; neurology; psychology; urogenital disease;
KW reproductive dysfunction; sexual dysfunction; cancer; tissue repair;
KW dermatology; skin pigmentation; photoaging; frailty; osteoporosis;
KW metabolic disease; cardiovascular disease; sleep disorder; hair loss;
KW gastrointestinal disease; anti-infection; sensory organ disorder; ss.
XX
OS Homo sapiens.
XX
```

FH Key Location/Qualifiers
 FT CDS 1..918
 FT /tag= a
 FT /product= "PFI-021"
 XX
 XX EPI225183-A2.
 XX
 XX
 PD 24-JUL-2002.
 XX
 XX
 PF 09-JAN-2002; 2002EP-00250128.
 XX
 XX
 PR 23-JAN-2001; 2001GB-00001739.
 XX
 PA (PFI2) PFIZER LTD.
 XX (PFI2) PFIZER INC.
 XX
 PI Harland L;
 XX
 DR WPI; 2002-601226/65.
 XX P-PSDB; AAG79446.
 PT New human G-protein coupled receptor involved in signal transduction,
 XX useful to treat disorders associated with its expression or activity, such
 XX as inflammation, allergy and cancer.
 PS
 XX
 XX Claim 1; Fig 1; bnp; English.
 CC This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.
 CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA
 CC libraries from peripheral blood mononuclear cells. Two ESTs have been
 CC identified in libraries derived from breast mRNA. PFI-021 and the
 CC corresponding cDNA are used to treat a patient needing altered activation
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,
 CC neurology, psychology, urogenital disease, reproductive and sexual
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin
 CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-
 CC infection, sensory organ disorders, sleep disorders and hair loss
 XX
 XX Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
 SQ
 Query Match 54.4%; Score 916.4; DB 6; Length 918;
 Best Local Similarity 99.9%; Pred. No. 3.3e-259;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 171 ATGCTGGCCACATACCTCCAGAAATTCCTTCGATCCTATAGTACACCCCACTTA 230
 DB 1 ATGCTGGCCACATACCTCCAGAAATTCCTTCGATCCTATAGTACACCCCACTTA 60
 QY 231 ATGAGCCCTCTACTTATAGTGTATTGCGGGGCTGGTGTGATTTCCATTCTTTTC 290
 DB 61 ATCAGCCCTCTACTTATAGTGTATTGCGGGGCTGGTGTGATTTCCATTCTTTTC 120
 QY 291 CTCCTGTGAAATATGAACCCGGTCACTGACCAACATGCGGGTCACTTAATCTTGGTGTG 350
 DB 121 CTCCTGTGAAATATGAACCCGGTCACTGACCAACATGCGGGTCACTTAATCTTGGTGTG 180
 QY 351 GTCCACAGCGTTTTCCTGCTGACAGTGCATTTCGCTTACCTTACCTCATCAAGAAACT 410
 DB 181 GTCCACAGCGTTTTCCTGCTGACAGTGCATTTCGCTTACCTTACCTCATCAAGAAACT 240
 QY 411 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 470
 DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 300
 QY 471 CTCAGGTTCTATTATGATGATGATCCGTCACAGATTCCTATCTTCTCAAGTGC 530
 DB 301 CTCAGGTTCTATTATGATGATGATCCGTCACAGATTCCTATCTTCTCAAGTGC 360
 QY 531 AAAGCAAAAGTGAATTTTACAGAAATGACATGCTGTGGTCCAGTGTCCAGATGTGG 590
 DB 361 AAAGCAAAAGTGAATTTTACAGAAATGACATGCTGTGGTCCAGTGTCCAGATGTGG 420

QY 591 ACGTGTGATGTGATTCATTTGGTACCCCTGGTGTCTCCGGTATGAAATCCATGAGGAA 650
 DB 421 ACGTGTGATGTGATTCATTTGGTACCCCTGGTGTCTCCGGTATGAAATCCATGAGGAA 480
 QY 651 TACAATGAGAGACCTGTTTAAATTTCAACAAGCTTGTGCTTACATATGTGAAATC 710
 DB 481 TACAATGAGAGACCTGTTTAAATTTCAACAAGCTTGTGCTTACATATGTGAAATC 540
 QY 711 ATCAACTATATGATGATTCATTTTGTGATACCGCTGTGTGATTCGTTGGTCTTCCAG 770
 DB 541 ATCAACTATATGATGATTCATTTTGTGATACCGCTGTGTGATTCGTTGGTCTTCCAG 600
 QY 771 GTCCTCATCATTTATGATGATGATGACAGAGCTACGCCACTTCTTACTATCCACAGAG 830
 DB 601 GTCCTCATCATTTATGATGATGATGACAGAGCTACGCCACTTCTTACTATCCACAGAG 660
 QY 831 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGAGGCTCATCTGTTGTTTCCTTCCC 890
 DB 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGAGGCTCATCTGTTGTTTCCTTCCC 720
 QY 891 TACCAAGTTCTTTAGATCTATTTACTTGAATGTTGTAGCGATTCGAATGCTGTAGAC 950
 DB 721 TACCAAGTTCTTTAGATCTATTTACTTGAATGTTGTAGCGATTCGAATGCTGTAGAC 780
 QY 951 AAGGTGCATTTTATACGAAATCTTCTGAGCTTAACAGAAATTAAGTGTATGATTTG 1010
 DB 781 AAGGTGCATTTTATACGAAATCTTCTGAGCTTAACAGAAATTAAGTGTATGATTTG 840
 QY 1011 CTTCCTTTGCTTTGGGGGAGGCAATGTTTAAAGAAAAGATATTTGGCTTATGAAAT 1070
 DB 841 CTTCCTTTGCTTTGGGGGAGGCAATGTTTAAAGAAAAGATATTTGGCTTATGAAAT 900
 QY 1071 TGTGTTTGTGCGCTTAG 1088
 DB 901 TGTGTTTGTGCGCTTAG 918
 RESULT 14
 ABT04867
 ID ABT04867 standard; cDNA; 918 BP.
 XX
 AC ABT04867;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 XX Human G protein coupled receptor hrUP29 coding sequence.
 DE
 XX Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
 KW hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX MO200242461-A2.
 PN
 XX
 PD 30-MAY-2002.
 XX
 XX 26-NOV-2001; 2001WO-US044386.
 PF
 XX
 XX 27-NOV-2000; 2000US-0253404P.
 PR 12-DEC-2000; 2000US-025536P.
 PR 20-FEB-2001; 2001US-0270286P.
 PR 20-FEB-2001; 2001US-0270286P.
 PR 06-APR-2001; 2001US-0282032P.
 PR 06-APR-2001; 2001US-0282356P.
 PR 06-APR-2001; 2001US-0282358P.
 PR 06-APR-2001; 2001US-0282358P.
 PR 14-MAY-2001; 2001US-0290917P.
 PR 31-JUL-2001; 2001US-0309208P.
 XX
 XX (AREN-) ARENA PHARM INC.
 PA
 XX
 PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX

DR WPI; 2002-566565/60.
DR P-PSDB; ABJ04069.
XX Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
PT agonists or antagonists for use as therapeutic agents.
XX
PS Claim 7; Page 56-57; 84bp; English.
CC The present invention provides the protein and coding sequences of
CC several human G-protein coupled receptors (GPCRs). These can be used in
CC the identification of candidate compounds as receptor agonists or inverse
CC agonists having applicability as therapeutic agents. The present sequence
CC is a GPCR coding sequence of the invention
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Query Match 54.4%; Score 916.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 3.3e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 171 ATGCTGGCCCAATACCTCCAGGAATCTCTTGGCATCTCTATAGACACCCCACTTA 230
DB 1 ATGCTGGCCCAATACCTCCAGGAATCTCTTGGCATCTCTATAGACACCCCACTTA 60
QY 231 ATCAGCTCTACTCATAGTCTTATTTGGCGGGCTGGGTGTCATTTCCATTCTTTTC 290
DB 61 ATCAGCTCTACTCATAGTCTTATTTGGCGGGCTGGGTGTCATTTCCATTCTTTTC 120
QY 291 CTCTGTGTAATAAGAACCCGGTCAGTGACACCAATGCGGTGTCATTAAGTGTGTC 350
DB 121 CTCTGTGTAATAAGAACCCGGTCAGTGACACCAATGCGGTGTCATTAAGTGTGTC 180
QY 351 GTCCACAGCGTTTTCGTGTCAGTGCCATTGCTTGACCTTCACTCACTCAAGAACT 410
DB 181 GTCCACAGCGTTTTCGTGTCAGTGCCATTGCTTGACCTTCACTCACTCAAGAACT 240
QY 411 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGTCATGTCACATCCATGTAC 470
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGTCATGTCACATCCATGTAC 300
QY 471 CTCAAGTCTTATTTATGTGTGTCATCTGTGTCACCAAGATCTCTATCTTCAAGTC 530
DB 301 CTCAAGTCTTATTTATGTGTGTCATCTGTGTCACCAAGATCTCTATCTTCAAGTC 360
QY 531 AAAGCAAAAGTGAATCTTACAGAAACTGTGATCTGTGTCAGTGTGTCAGTGTG 590
DB 361 AAAGCAAAAGTGAATCTTACAGAAACTGTGATCTGTGTCAGTGTGTCAGTGTG 420
QY 591 ACGCTGGATTTGTCATTTGTGTCACCCCTGTTCTCCCGTATGGAATCATAGAGAA 650
DB 421 ACGCTGGATTTGTCATTTGTGTCACCCCTGTTCTCCCGTATGGAATCATAGAGAA 480
QY 651 TACATGAGAGACACTGTTTAAATTTCAAAAGAGCTGCTTACATATGTGAAATC 710
DB 481 TACATGAGAGACACTGTTTAAATTTCAAAAGAGCTGCTTACATATGTGAAATC 540
QY 711 ATCAACTATATGATGATCTTTGTGTCATAGCCGTTGTGATCTGTTGTCATTCAG 770
DB 541 ATCAACTATATGATGATCTTTGTGTCATAGCCGTTGTGATCTGTTGTCATTCAG 600
QY 771 GTCTTCATCATTTATGTTGATGTCAGAGTCAAGCCATCTTACTATCCACAGAG 830
DB 601 GTCTTCATCATTTATGTTGATGTCAGAGTCAAGCCATCTTACTATCCACAGAG 660
QY 831 TTCTGGGCTCAGCTGAAAACTATTTTATATAGGGGTCACTCTGTTGTTCTTCC 890
DB 661 TTCTGGGCTCAGCTGAAAACTATTTTATATAGGGGTCACTCTGTTGTTCTTCC 720
QY 891 TACAGTTCTTAGATCTATTAAGTGTGAAAGTGTGAGCAATTCCTGTAGAGC 950
DB 721 TACAGTTCTTAGATCTATTAAGTGTGAGCAATTCCTGTAGAGC 780

QY 951 AAGTTGCATTTTATACGAAATCTTGTAGATGTAACAGCAATTAGCTGTATGTTG 1010
DB 781 AAGTTGCATTTTATACGAAATCTTGTAGATGTAACAGCAATTAGCTGTATGTTG 840
QY 1011 CTCTCTTTTGTCTTTTGGGGAGCCATTGTTTAAAGCAAAATTAATTGCTTATGGAAT 1070
DB 841 CTCTCTTTTGTCTTTTGGGGAGCCATTGTTTAAAGCAAAATTAATTGCTTATGGAAT 900
QY 1071 TGTGTTTGTGCGGTAG 1088
DB 901 TGTGTTTGTGCGGTAG 918
RESULT 15
ABZ59171
ID ABZ59171 standard; DNA; 918 BP.
AC ABZ59171;
XX 28-APR-2003 (first entry)
DT
XX Human TGR343 protein encoding DNA.
DE
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotoxic;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory; gene; de.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /*tag= a
FT /product= "TGR343"
XX
XX WO200304678-A2.
XX 16-JAN-2003.
XX
XX 01-JUL-2002; 2002W0-US020860.
XX
XX 03-JUL-2001; 2001US-0302800P.
XX
XX (TULAR-) TULARIK INC.
XX
XX Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX WPI; 2003-210368/20.
DR P-PSDB; ABP71378.
XX
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.
XX
XX
PS Claim 7; Page 61; 74bp; English.
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombinant methodology. The polypeptides are useful for screening or
CC identifying modulators of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperlactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR343
CC protein encoding DNA
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 54.4%; Score 916.4; DB 8; Length 918;
 Best Local Similarity 99.9%; Pred. No. 3.3e-259;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	171	ATGCTGGGCAATAATCCCTGAGAAATTCCTTCGATCCCTATAGTACACCCCACTTA	230
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QY	231	ATCAGCCTCTACTTATAGTCTTATGCGGGCTGATGGGATCATTTCCATTCCTTTTC	290
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QY	291	CTCCTGTGAAAATGAACACCGGTCAGTACACCATGCGCGTCATTAACTTGTGTGNG	350
DB	121	CTCCTGTGAAAATGAACACCGGTCAGTACACCATGCGCGTCATTAACTTGTGTGNG	180
QY	351	GTCCACAGCTTTTCTGTGACATGCGCATTTGCTTGAACCTTCACTCAAGAACT	410
DB	181	GTCCACAGCTTTTCTGTGACATGCGCATTTGCTTGAACCTTCACTCAAGAACT	240
QY	411	TGATGTGAGGCTGCGCTTCGAAATTTGTAGTGCATGTCACATCCACATGATAC	470
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QY	471	CTCAGTTCCTATTCTATGTGTGATCCTGTGCACAGATACTCATCTTCTCAAGTGC	530
DB	301	CTCAGTTCCTATTCTATGTGTGATCCTGTGCACAGATACTCATCTTCTCAAGTGC	360
QY	531	AAAGCAAGTGAATTTTACAGAAATCTGATGCTGTGCTGCCAGTGTGGCATGTGG	590
DB	361	AAAGCAAGTGAATTTTACAGAAATCTGATGCTGTGCTGCCAGTGTGGCATGTGG	420
QY	591	ACGCTGTGATGTCATTTGTGGTACCCGTTGTCTCCGGTATGAAATCCATGAGGA	650
DB	421	ACGCTGTGATGTCATTTGTGGTACCCGTTGTCTCCGGTATGAAATCCATGAGGA	480
QY	651	TACAATGAGAGCACTGTTTAAATTTCAAAAGCTTGTCTTACATATGTGAAATC	710
DB	481	TACAATGAGAGCACTGTTTAAATTTCAAAAGCTTGTCTTACATATGTGAAATC	540
QY	711	ATCAACTATATGATGATGATTTTGTCTATAGCCGTTGCTGTGATTTGTGCTTCAG	770
DB	541	ATCAACTATATGATGATGATTTTGTCTATAGCCGTTGCTGTGATTTGTGCTTCAG	600
QY	771	GTCCTCATATATGATGATGATGAGAGCTAGGCCACTTTTACTATATCCACAGAG	830
DB	601	GTCCTCATATATGATGATGATGAGAGCTAGGCCACTTTTACTATATCCACAGAG	660
QY	831	TTCTGGGCTCAGTGAATAAATTTTATAGGGGTCATCTTGTGTTTCTTCCC	890
DB	661	TTCTGGGCTCAGTGAATAAATTTTATAGGGGTCATCTTGTGTTTCTTCCC	720
QY	891	TACCAATTCCTTAAAGATCTATTAATGATGAGCATTCGAATGCTGTAGCAGC	950
DB	721	TACCAATTCCTTAAAGATCTATTAATGATGAGCATTCGAATGCTGTAGCAGC	780
QY	951	AAAGTGTGATTTTAAAGAAATCTTCTGAGTGAACGAATTAAGTGTATGATTTG	1010
DB	781	AAAGTGTGATTTTAAAGAAATCTTCTGAGTGAACGAATTAAGTGTATGATTTG	840
QY	1011	CTTCTCTTTTCTTTGGGGGAAGCATGTTTAAAGCAAAAGATATGCTTATGGAAT	1070
DB	841	CTTCTCTTTTCTTTGGGGGAAGCATGTTTAAAGCAAAAGATATGCTTATGGAAT	900
QY	1071	TGAGTTTGTGCGGTAG 1088	
DB	901	TGAGTTTGTGCGGTAG 918	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:36:04; Search time 305.598 Seconds
(without alignments)
9016.710 Million cell updates/sec

Title: US-10-085-233B-1

Perfect score: 1684

Sequence: 1 tcgacagctgcacacattt.....ctatgcagctgcgcgcgcg 1684

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76.4	4.5	1113	US-09-826-509-540	Sequence 540, App
2	76.4	4.5	1805	US-08-405-271A-18	Sequence 18, Appl
3	76.4	4.5	1973	US-09-016-434-1391	Sequence 1391, Ap
4	76.4	4.5	1973	US-09-022-655-1417	Sequence 1417, Ap
5	76.4	4.5	3205	US-09-976-594-171	Sequence 171, Appl
6	73.2	4.3	1134	US-09-743-871B-14	Sequence 14, Appl
7	70.2	4.2	1177	US-09-743-871B-13	Sequence 13, Appl
8	62.8	3.7	1273	US-09-910-695-9	Sequence 9, Appl
9	59.8	3.6	1330	US-08-147-592A-5	Sequence 5, Appl
10	59.8	3.6	1330	US-08-292-694A-5	Sequence 5, Appl
11	59.8	3.6	1567	US-08-889-108-16	Sequence 16, Appl
12	59.8	3.6	1567	PCT-US94-10358-16	Sequence 16, Appl
13	59.8	3.6	2600	US-08-986-209A-1	Sequence 1, Appl
14	59.8	3.6	2706	US-08-454-549-1	Sequence 1, Appl
15	59.8	3.6	2706	US-08-454-552-1	Sequence 1, Appl
16	59.8	3.6	2706	US-08-676-351-1	Sequence 1, Appl
17	59.4	3.5	1143	US-09-826-509-542	Sequence 542, App
18	59.4	3.5	1182	US-09-016-434-1417	Sequence 1417, Ap
19	58.2	3.5	1452	US-08-149-093A-3	Sequence 3, Appl
20	58.2	3.5	1452	US-08-911-245-3	Sequence 3, Appl
21	58.2	3.5	1452	US-08-553-058C-3	Sequence 3, Appl
22	58.2	3.5	1452	US-08-514-451A-3	Sequence 3, Appl
23	58.2	3.5	1452	US-09-170-331-3	Sequence 3, Appl
24	58.2	3.5	1452	US-09-510-473-3	Sequence 3, Appl
25	58.2	3.5	1452	US-09-048-916B-3	Sequence 3, Appl
26	58.2	3.4	1002	US-09-170-496D-15	Sequence 15, Appl
27	58.2	3.4	1002	US-09-170-496D-171	Sequence 171, App

28	58	3.4	1518	1	US-08-148-215A-3	Sequence 3, Appl
29	58	3.4	1518	4	US-09-016-434-1480	Sequence 1480, Ap
30	57.8	3.4	1142	3	US-08-765-743-1	Sequence 1, Appl
31	57.8	3.4	1143	4	US-09-341-446B-1	Sequence 1, Appl
32	57.8	3.4	1284	4	US-09-341-446B-3	Sequence 3, Appl
33	55	3.3	1000	3	US-08-147-592A-11	Sequence 11, Appl
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35	54.2	3.2	1155	3	US-09-053-866-3	Sequence 3, Appl
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37	54.2	3.2	1155	4	US-09-472-130A-3	Sequence 3, Appl
38	54	3.2	1257	4	US-09-826-509-572	Sequence 572, App
39	54	3.2	1296	1	US-07-816-283-9	Sequence 9, Appl
40	54	3.2	1296	1	US-08-417-103-9	Sequence 9, Appl
41	54	3.2	1413	4	US-09-016-434-1321	Sequence 1321, Ap
42	52	3.1	1223	4	US-09-743-871B-11	Sequence 11, Appl
43	52	3.1	1283	4	US-09-743-871B-12	Sequence 12, Appl
44	50.4	3.0	1256	4	US-09-743-871B-9	Sequence 9, Appl
45	50.4	3.0	2634	4	US-09-743-871B-8	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-09-826-509-540
Sequence 540, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruhema, Karin
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826, 509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 540
LENGTH: 1113
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-509-540

Query Match      4.5%; Score 76.4; DB 4; Length 1113;
Best Local Similarity 46.7%; Pred. No. 8.6e-13;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Oy 264 CTGTGTGCTGCTCATTTTCATTTCTTCTCTGCTGTAAGTAAGACCGGTGATGACC 323
Db 199 CTGGGAGACGCTCTTGTCATGTCATGTCATCTTCAAGCAGCAACAAAGAGAGCCACC 258

Oy 324 ACCATGCGGCTCATTTAATTGCTGTGTGCTCAGAGCTTTTGTCTGACAGTCCATTT 383
Db 259 AATATTATCATCTTTAATCCTGCGCCCTGCGGAGACACTGTGCTCTGAGAGCTGCCCTTC 318

Oy 384 CGCTTGACCTCACTCATCAAGAAAGACTGGATGTTGGGCTGCCCTTGTGCAATTGTG 443
Db 319 CAGGCGACGAGCATCTCCCTGCGCTTCTGCGCCCTTGGGGAATCGCTGTGCAAGACAGTC 378

Oy 444 AGTGCATGCTGACATCCACATGATACCTTCACTTATGATGATGATGATGATGATGATG 503
Db 379 ATTGCATTATCACTTACATCAATGATGATGATGATGATGATGATGATGATGATGATG 438

Oy 504 ACCAGATACCTCATCTTCTTCAAGTCAAGAAAGCAAGAAAGTGAATTTTACAGAAATGCA 563
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Oy 564 GCTGTGCTGCTCAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 623
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Db 499 GCCCAGGCTGTCATGTCGTCATCTGGGCCCTGTCCTGTGTGCGTGTCCCGTGGC 558
Qy 624 GTCTCCCGGTATGGAATCCATGAGGAAATACATGAGAGCACTGTTTAAATTTCACAA 683
Db 559 ATCATGGGCTCGGACAGGTGAGAGATGAGATCGCTGTGAGATCCCTACC 618
Qy 684 GAGCTTGCTTACATATGTAATAATCATCAATATGATGATCTTTTGTGATGCC 743
Db 619 CCTAGAGATTACGGGGCCGGGTGTGGCCATGTCATCTTCTCTCTCATGTC 678
Qy 744 GTTGTGATTCGTGTGCTTCCTCAGGTCTTCATCAT 781
Db 679 CCCGTGCTGTCATCTGTCTGCTACAGCTCATGAT 716

RESULT 2
US-08-405-271A-18
; Sequence 18, Application US/08405271A
; Patent No. 6432652
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & ROEBSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,271A
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526, 22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNPOBRSMSH
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1119
; US-08-405-271A-18

Query Match 4.5%; Score 76.4; DB 3; Length 1805,
Best Local Similarity 46.7%; Pred. No. 1,2e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
Qy 264 CTGCTGGGTGATTCATTCATCTTTCTCTGTGAAATGAACCCGGTCAGTACC 323
Db 208 CTGGGGAAGCTGCTGTATGATGATCTCTCAAGGACACCAAAATGAAGACGCCACC 267
Qy 324 ACCATGGCGGTCAATTAATCTGTGTGTGTCACAGCCGTTTCTGCTGACAGTGCATTT 383
Db 268 AATATTATTCATCTTTTAACTGGCCCTGGCCGACACTGTGTCGTGCTGACGCTGCCCTTC 327
Qy 384 CGCTTGACCTACCTCATGACGAAGACTTGATGTTTGGGCTGCCCTTCTGCAAAATTGTG 443

Db 328 CAGGACCGGACATCTCTCGGGCTTCTGGCCGTTTGGGAATGCGCTGTGCAAGACAGTC 387
Qy 444 AGTGCATGCTGCACATTCACATGTAATCTCAGCTTCTATTCTATGTGATCTCGTGC 503
Db 388 ATGACCATGATCACTACAAATGTTTCACACAGACCTTACCTCACTCCATGAGTGTG 447
Qy 504 ACCAGATACCTCATCTTCTTCAAGTGCACAAAGACAAAGTGAATTTACAGAAACTGCAT 563
Db 448 GATGCTATGTAACCATCTGTCACCCATCCGTCCTGAGGTCCGACGTCCAGACAA 507
Qy 564 GCTGTGCTCCAGTCTGACATGTCAGCGTGTGATTTGTATTTGTATCCCTGTT 623
Db 508 GCCCAGGCTGTGATGTGGGCATCTGGGCCCTGGCTGTGTGTGCGTTCGCCGTGGCC 567
Qy 624 GTCTCCCGGTATGGAATCCATGAGGAAATACATGAGAGCACTGTTTAAATTTCACAA 683
Db 568 ATCATGGGCTCGGACAGGTGAGATGAAAGATGAGTGGCTGTGAGATCCCTACC 627
Qy 684 GAGCTTGCTTACATATGTAATAATCATCACTATATGATGATCTTTTGTATAGCC 743
Db 628 CTTAGGATTTACTGGGGCCCGGTGTTGCCATCTGCATCTTCTCTTCTCTTATGTC 687
Qy 744 GTTGTGATTCGTGTGCTTCCTCAGGTCTTCATCAT 781
Db 688 CCCGTGCTGTCATCTGTCTGCTACAGCTCATGAT 725

RESULT 3
US-09-016-434-1391
; Sequence 1391, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: g471316
US-09-016-434-1391

US-09-016-434-1391

Query Match	4.5%	Score 76.4;	DB 4;	Length 1973;
Best Local Similarity	46.7%;	Pred. No. 1.3e-12;		
Matches 242;	Conservative 0;	Mismatches 276;	Indels 0;	Gaps 0;

Qy	264	CTGGGGGGTGCATTTTCATCTTTTCCCTGGTGTAAATGAACCCGGGTAGAGAC	323
Db	376	CTGGGGAACCTGCTTGTTCATGTACGTATCTTCAGGCAACCAAAATGAAGACGCACC	435
Qy	324	ACCATGGCGGTCAATTAACTTGGTGGTGTCCACAGCGTATTTCTGCTGCAGTGCATT	383
Db	436	AATATTACATCTTTAACTCGGCCCTGGCCGACACCTCTGTCTGTACGCTGCCCTTC	495
Qy	384	CGCTTGACCTTACCTTCATCAAGAAAGCTTGGATGTTGGGCTGCGCTTCTGCAATTTGTG	443
Db	496	CAGGGCAAGGACATCTCCTCGGGCTTTCGGCGTTCGGAAATGCGCTGGCAAGACAGTC	555
Qy	444	AGTGGCAATGCTGCACATGCATGTACCTCAGCTTCCTATTCTATGTGGTGAATCTGGTTC	503
Db	556	ATTGCGATTGACTACTTACACAACTGTTCACACACACCTTCACTCCATGAGTGTG	615
Qy	504	ACCAGATATCCATCTTCTCTCAAGTGCAAAGCAAAAGTGAATTTCAAGAAACGTGCAT	563
Db	616	GATGCGTATGTAGCCATCTGCGACCCCATCGGTCCCTTGACGTGCGACGTCCAGCAAA	675
Qy	564	GCTGGGCTGCAGAGTGTGCATGTGACGCTGTGATATGTCAATGTGGTACCCCTGGTT	623
Db	676	GCCCAAGGTGTCAATGTGGCCATCTGGGCGCTCGCTCTGTGTGTGCGATTTCCCGTTGCC	735
Qy	624	GTCCTCCGGTATGGAATCCATGAGGAATTAACAATGAGAGCACCTGTTTAAATTTCAAAA	683
Db	736	ATCATGGGCTCGGCAAGATCGAGATGAAGATGCAATGCTGGTGAAGATCCCTAAC	795
Qy	684	GAGCTGTCTTACACATATGTGAAAAATCATCACTATATATATGTCAATTTTGTCAAGCC	743
Db	796	CCTCAGGATTAATGCGGCGCCGGTGTGTTGGCACTGTGATCTTCTCTTCCTTCATCGTC	855
Qy	744	GTTGCTGTGATTTCTGTGGTCTTCCAGGCTTCATCAT	781
Db	856	CCCGTCTGTGCATCTCTGTCTGTGCACAGCTTCATGAT	893

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1      RESULT 4
2      US-09-023-655-1417
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4      : Sequence 1417, Application US/09023655
5      : Patent No. 6607879
6      :
7      : GENERAL INFORMATION:
8      :
9      : APPLICANT: Cocks, Benjamin G.
10     :
11     : APPLICANT: Susan G. Stuart
12     :
13     : APPLICANT: Jeffrey J. Sellhammer
14     :
15     : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENES
16     :
17     : TITLE OF INVENTION: EXPRESSION
18     :
19     : NUMBER OF SEQUENCES: 1508
20     :
21     : CORRESPONDENCE ADDRESS:
22     :
23     : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
24     :
25     : STREET: 3174 PORTER DRIVE
26     :
27     : CITY: PALO ALTO
28     :
29     : STATE: CALIFORNIA
30     :
31     : COUNTRY: USA
32     :
33     : ZIP: 94304
34     :
35     : COMPUTER READABLE FORM:
36     :
37     : MEDIUM TYPE: Floppy disk
38     :
39     : COMPUTER: IBM PC compatible
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41     : OPERATING SYSTEM: PC-DOS/MS-DOS
42     :
43     : SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
44     :
45     : CURRENT APPLICATION DATA:
46     :
47     : APPLICATION NUMBER: US/09/023,655
48     :
49     : FILING DATE: HEREWITH
50     :
51     : CLASSIFICATION:
52     :
53     : PRIOR APPLICATION DATA:
54     :
55     : APPLICATION NUMBER:

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1 FILING DATE:
2 CLASSIFICATION:
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Zeller, Karen J.
5 REGISTRATION NUMBER: 37,071
6 REFERENCE/DOCKET NUMBER: PA-0001 US
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (650) 855-0555
9 TELEFAX: (650) 845-4166
10 INFORMATION FOR SEQ ID NO: 1417:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 1973 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 IMMEDIATE SOURCE:
17 LIBRARY: GENBANK
18 CLONE: g471116
19
20 JS-09-023-655-1417

Query Match 4.5%; Score 76.4; DB 4; Length 1973;
Best Local Similarity 46.7%; Pred. No. 1,3e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy 264 CTGGTGGGTGCATTTCCATTTCTTTCTCTCTGGTGAATAAGAACACCCGGTCAGTACC 323
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Db 376 CTGGGGAACCTGCTTGTGATGTACGTCACTCTCAGGCGACACCAAAATGAAAGCAGCCACC 435
|||
Qy 324 ACCATGGCGGTCATTAACTTGTGTGTGTCCAGCGCTTTTCTGCTGACATGGCCATT 383
|||
Db 436 AATATTTCATCTTTAACCTGGCCCTGGCGGACACTGTGTCTGTGAAGCTGCCCTTC 495
|||
Qy 384 CGCTTGAACCTTACCTTCATCAAGAAAGACTTGAATGTTTGGGCTGCGCTTCGCAAAATTTGTG 443
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Db 496 CAGGGGACAGCAATCTCTCTGGGCTTCTGGCCGTTTGGGAATGGCCTGTGCAAGACAGTTC 555
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Qy 444 AGTGCATGTGCAACATCCACATGTAAGTCACTCACTTCTTAATGTATGGTATCCTGATC 503
|||
Db 556 ATTGCATTTGACTACTACCAACATGTTTCAACGACACTTCACCCCTAATGCCATGAGTGTG 615
|||
Qy 504 ACCAGATTAACCTCATCTTCTTTAAGTGCAAAGCAAAAGTGAATTTTACAGAAAATCTGAT 563
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Db 616 GATGCGATATGAGGCATCTTGCACCCCATCCGTGCCCTCGAAGCTCGGACGTCAGCAAA 675
|||
Qy 564 GCTGAGGCTGCAGAGCTGGCATGTGAGCGGCTGGATTTGATTTGGGTACCCCGTGT 623
|||
Db 676 GCCCAGGCTGTCAATGAGCCATCTGGGCCCTTGGCTCTGTGTGTGGGTTCGCCGTGCC 735
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Db 736 ATCATGGGCTCGGCAAGGTGAGAGATGAAGATGAGATGCTGTGAGATTCCTTACC 795
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Qy 684 GAGCTTGCTTACATATATGAAAAATCATCACTATATGATATGATTTTGTCTATGCC 743
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Db 796 CCTAGGATTACTGAGGCGCCGCTGTGGCCATCTGCATCTTCTCTTCATCTGTC 855
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Qy 744 GTTGTGTGATTTCTTGTGTCTTCCAGGCTTTCATCAT 781
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Db 856 CCCGTGCTGTCACTCTGTCTGTCAAGCCCTCATGAT 893
|||

RESULT 5
US-09-976-594-171
; Sequence 171, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: P-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409

Db 277 GCACACCAAAATGAGACAGCCACCAATATTATCTTTAACTGCGCCCTGGCCGACAC 336
Qy 359 CGTTTTCGCTGACAGTGGCAATTTGGCTTACCTACCTCAAGAAAGCTTGATTT 418
Db 337 TCTGCTCTGCTGACGCTGCTCTTCAAGGACGAGCAATCTCTGGGCTTCTGGCCGTT 396
Qy 419 TGGGCTGCTCTCTGCAATTTGTGATGCGCATGCTGACATCCACATGATACCTGCTT 478
Db 397 TGGGAATGCGCTGTCAGACAGATGATGCTTACCTAATCAACATGTTTACACGAC 456
Qy 479 CCTATTATGATGATGATCTGCTGTCACAGATACCTCATCTTTTCAAGTGCAGAACAA 538
Db 457 CTTCACCTTAACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 516
Qy 539 AGTGAATTTCAAGAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
Db 517 CCTGACGCTGCGACGCTGCGACGAGGCTGCTGATGATGATGATGATGATGATGATGATG 576
Qy 599 GATTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
Db 577 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
Qy 659 GAGACACTGTTTAAATTTCAAAAGAGCTTGTACATATGATGAAATCATCACTA 718
Db 637 CGAGTGCCTGCTGAGATGCTTACCTTACGAGATGATGAGGAGGCTGCTGCTGCTGCTG 696
Qy 719 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
Db 697 CATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
Qy 779 CAT 781
Db 757 GAT 759

RESULT 8
US-09-910-695-9
Sequence 9, Application US/09910695
Patent No. 6737252
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Vicar, Alain P.
Zlotnik, Albert
TITLE OF INVENTION: Mammalian Chemokines; Receptors;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/910,695
FILING DATE: 20-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/122,585
FILING DATE: 24-Jul-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0757
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1273 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 429..1238
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 60/053,693
FILING DATE: 25-Jul-1997
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-910-695-9

Query Match 3.7%; Score 62.8; DB 4; Length 1273;
Best Local Similarity 45.7%; Pred. No. 1.5e-08;
Matches 255; Conservative 0; Mismatches 302; Indels 1; Gaps 1;

Qy 227 CTTAATCAGCTCTTACTTATGATGCTTATTTGGCGGCTGGTGGTGCATTTTCATTTCT 286
Db 321 CTTAGTCTTTTACAGCTGCAATCTTCTGATTTGGCTGTGTTGTTATGATGATGATGATG 380
Qy 287 TTTCTCTGCTGAAATGAAACACCGGTCAGTACACCAATGCGGTCATTAACTTGT 346
Db 381 GGTTTTACGCTGTAAGACCAAGAAAGAACAG-TCACATCTTACATGATGAACGTTGC 439
Qy 347 GGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTCATCAAGAA 406
Db 440 ACTACTGAGCTGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 499
Qy 407 GACTTGATGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 466
Db 500 CGAGTGCATTTGAGAGTACTTCTGCAATCTTGGGAGCCCTGCTGCTGCTGCTGCTGCTG 559
Qy 467 GTACCTCAGCTCTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 526
Db 560 AAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
Qy 527 GTGCAAGACAAAGTGAATTTTACAGAAATGATGATGATGATGATGATGATGATGATG 586
Db 620 GCCAAATATGCAAGAGGCTGAAAGAACACCGGAGGCGGTGCTGCTGCTGCTGCTGCTG 679
Qy 587 GTGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 646
Db 680 CTGGGTATGACCTTGCACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
Qy 647 GGAATACAAAGAGAGACGTTTAAATTTCAAAAGAGCTTGTACATATGATGAA 706
Db 740 TGCTCTCTCCCGGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Qy 707 AATCATCACTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 766
Db 800 CGTGTCACTTTCAGCGGATCATATTTTCTTCCGATCCCTTGTGATCATGATCGG 859
Qy 767 CCAAGTCTTCAATTAAT 784
Db 860 GTGCTAGTGTGATCAT 877

RESULT 9
US-08-147-592A-5
Sequence 5, Application US/08147592A
Patent No. 6096513
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
TITLE OF INVENTION: Opioid Receptor Genes,
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 161..1261
US-08-147-592A-5

Query Match 3.6%; Score 59.8; DB 3; Length 1330;
Best Local Similarity 44.8%; Pred. No. 1.4e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

QY 179 CCAGAAATACCTCCAGAGATTCCTTGGGATCCTATAGTGACACCCCACTTAATACCT 238
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DB 262 CCTCAATGCTAGCCACAGTGCCTTCCGCCCTTGACTCAAGGTCAACATCGGGGCT 321
|||
QY 239 CTACTTCATAGTGTCTTATTTGGCGGGCTGTTGGG--TGTCAATTCATTCCTTTCCCTCT 295
|||
DB 322 CTACTTGGCTGTGTGCAATCGGGGGCTCTCGGGAACTGCTCTGTAATGATGTCATCT 381
|||
QY 296 GGTGAAATGAAACCCGGTCAAGTACACCAATGGCGTCAATTAATGTTGTGTGTCCA 355
|||
DB 382 CAGGCAACCAAGATGAAGACTGCTACCAATTTAATATGATGGAGCTGA 441
|||
QY 356 CAGCGTTTTCGTGACAGTGCATTCGCTTGAACCTACTATCAAGAAAGCTTGAT 415
|||
DB 442 TACCTGTGTCTGTGACACTGCCCCCTTCAGGGGACAGACATCCTTGTGGGCTTCTGCC 501
|||
QY 416 GTTTGGGCTGCCCTTGGCAAAATTTGTAGAGCATGCTGACATCAACATGATCCTCAC 475
|||
DB 502 ATTTGGGAATGACATGTGCAAGACGGTCAATGCTATGACTACATCAACATGTTTACAG 561
|||
QY 476 GTTCTATTCATGTGTGATCTCGTCAACAGATACCTCACTTCTTCAAGTCAAGA 535
|||
DB 562 CACTTCACTTGAAGTGCATGAGTGAAGACCGTTATGATGATCTGACCACTATCCG 621
|||
QY 536 CAAAGTGAATTTACAGAAAATGCAATGCTGTGTGCGCAAGTCTGGCATGTGACGCT 595
|||
DB 622 TGCCCTGATGTTGCGACATCAAGTAAAGCCAGGCGTTAATGTGACCATATGGGCTCT 681
|||

QY 596 GGTGATTCATGTGTGATACCCCTGGTGTCTCCCGTATGATATCCATGAGGAATACAA 655
|||
DB 682 GCGTGGGTGTGTGTGTCTTCTTCCATCATAGGCTCAGCAACAGTGAAGATGAAGA 741
|||
QY 656 TGAGAGCACTGTTTAAATTTCAAAAGACTTGCTTACATATGTAATAATCATCA 715
|||
DB 742 GATGAGTGTCTGTGAGATCCCGCCCTCAGAGCTATGGGGCCGTGATTTGCCAT 801
|||
QY 716 CTATATGATAGTATTTTGTCAATAGCGTGTGATGATTCGTGCTCCAGTCTT 775
|||
DB 802 CTGATCTCTCTTTTCTTCTTCAATCCCGGTTGATCATCTGTGTGCTACAGCT 861
|||
QY 776 CATCAT 782
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DB 862 CATGAT 868
|||

RESULT 10
US-08-292-694A-5
Sequence 5, Application US/08292694A
Patent No. 6319686
GENERAL INFORMATION:
APPLICANT: BELL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUDA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,694A
FILING DATE: August 19, 1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 5 No. 6319686ember 1993
FILING DATE: 08/147,592
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US94/05747
FILING DATE: 20 May 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARK B. WILSON
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 161..1261
US-08-292-694A-5

Query Match 3.6%; Score 59.8; DB 3; Length 1330;
Best Local Similarity 44.8%; Pred. No. 1.4e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

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QY 179 CCNAAATACCTCCAGAAATTCCTCTTGAGATCTATATGACACCCCACTTAACAGCT 238
DB 262 CCTAAATGCTACCAAGTGCCTTCCTGCCCCCTTGAGACTCAAGGTACCACTGAGGCT 321
QY 239 CTACTTCATAGTCTTATTTGCGGGCTGCTGGG---TGTCATTTTCAATTTCTTTCTCT 295
DB 322 CTACTTGCTGTGTGATCGGGGGCTCTCTGGGAACCTGCTGCTATATGATCACTCT 381
QY 296 GGTGAAATGAAACCCGGTCAAGTACCAACCATGCGGTCAATTAATTTGCTGCTGCA 355
DB 382 CAGGACACCAAGTAAAGACTGCTACCAATTTATTTATCTGCGACTGGCTGA 441
QY 356 CAGGCTTTTCTGTGACAGTCCATTTGCTTGAACCTCACTCAAGAAAGACTTGAT 415
DB 442 TACCTGCTCTGTGACACTGCCCCCTTCAGGGCAAGACATCTTCTGGGCTTCTGGCC 501
QY 416 GTTTGGGCTGCCCTTCGCAAAATTTGAGTGCATGTCGACATCCACATGTACTCCAC 475
DB 502 ATTTGGGAATGCACTGTGCAAGACGCTCATTTGCTATGCACTACACATGTTTACCG 561
QY 476 GTTCCATATTCATGTGTGATCTGTGACCAAGTACCTCATCTTCTTCAAGTCAAGA 535
DB 562 CACTTTCATTTGACTGCAATGAGTAAAGCGTTAGTATGATCTGCTGCAACCTTACCG 621
QY 536 CAAAGTGAATTTCAAGAAATGCACTGCTGTGCTGCGACGCTGCGCATGTGAGGCT 595
DB 622 TGCCCTTGATGTGACATCACTCAATTAAGCCAGCGCTTATATGTGCGCATATGCGCT 681
QY 596 GGTATTTGATGTGATGATCCCTGTTGCTCCCGGATGAAATTCATGAGAAATCAA 655
DB 682 GGTCTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY 656 TGAGGACACTGTTTAAATTTCAAAAGCTTGTCAACATATGTAAGTAATCATCA 715
DB 742 GATGAGTGCCTGTGAGATCCCGGCCCTCAGAGACTATGGGGCCCTGATTTGCGAT 801
QY 716 CTATATGATGATCTTTTGTGATGACCGCTGTGCTGCTGCTGCTGCTGCTGCTG 775
DB 802 CTGATCTTCTTTTCTTTCTTCAATCCCGTTCATCATCTGCTGCTGCTGCTGCT 861
QY 776 CATCAT 782
DB 862 CATCAT 868
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RESULT 11

US-08-889-108-16
; Sequence 16, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/305,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005\WIM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1567 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 173..1273

US-08-889-108-16

Query Match 3.6%; Score 59.8; DB 3; Length 1567;

Best Local Similarity 45.6%; Pred. No. 1.5e-07;

Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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QY 235 GCGCTACTCATAGTCTTATTTGGGGGCTGCTGGG---TGTCATTTCAATTTCTTCC 291
DB 330 GGGCTACTTGTGCTGTGTGATGAGGAGGCTCTCTGGGAACCTGCTGCTATGATGTCA 389
QY 292 TCCGTGAAATGAAACCCGGTCAAGTACCAACATGCGGCTATTAATTTGCTGCTG 351
DB 390 TCCGACAGGACACCAAGATGAAGACGCTACCAATTTATTTAATCTGGCACTGG 449
QY 352 TCCACAGCGTTTCTGTGCTGACAGTGCATTTGCTTGAACCTTCAAGAAAGCTT 411
DB 450 CTGATACCCCTGCTGTGCTTAACTGCTTCAAGGACAGACATCTTCTGCGCTTCT 509
QY 412 GGAATTTGGGCGCCCTTGCAGAAATTTGTAGTGCATGCTGACATCATCATGATAC 471
DB 510 GGGCATTTGGGAATGCACTGTGCAAGCTGTCAATGCTATGCACTATCAACATGTTTA 569
QY 472 TCACTTCTATTTCTATGTGTGATCTGTGCTGACAGATACCTCATCTTCTTCAAGTCA 531
DB 570 CCAAGCACTTTTACTGTGACCGCATGAGGCTAGACGGCTATGTGGCTATGCGAACCTTA 629
QY 532 AAGACAAAGTGAATTTCAAGAAATGCACTGCTGTGCTGCTGCTGCTGCTGCTGCA 591
DB 630 TCCGTGCCCTTGAATGTGCGACATCCAGCAAAAGCCAGGCTGTAAATGTGGCATATG 689
QY 592 CGCTGATGATTTGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
DB 690 CCGTGGCTTCAAGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 749
QY 652 ACAATGAGAGCACTGTTTAAATTTCAAAAGCTTGTCTTACATATGTAAGAAATCA 711
DB 750 AAGAGATCGAGTGCCTGTGAGATCCCGCCCTCAGAGACTATTTGGGGCCCTGATTTG 809
QY 712 TCAATATATGATGATCTTTTGTGATGACCGCTGTGCTGATCTGTTGCTTCCAGG 771
DB 810 CCAATGCACTTCTTTTCTTTCTTCAATCCCGTGTGATCATCTGCTGCTGCTGCTGCT 869
QY 772 TCTTCATCAT 782
DB 870 GCGTCATGAT 880
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RESULT 12

PCT-US94-10358-16
; Sequence 16, Application PC/TUS9410358

Db 820 GGCCTTCGGTGGTGGTGGTTCCTGTCATATAGGCGTCAGACAGATGGAGATGAGA 879
QY 656 TGAGAGACACTGTTTAAATTTACAAAGAGCTTGCTTACATATGGAATAATCATCA 715
Db 880 GATCAGAGCGCTGGTGGAGATCCCGCCCTCAGAGACTATGGGCGCCCTGATTTGCCAT 939
QY 716 CTATATGATAGTATTTTGTGTCATAGCGGTGCTGTGATTTCTGTGTCCTTCCAGTCTT 775
Db 940 CTGCATCTTCTTTTCTTTCTTCTTATCATCCGGTCTGATCATCTCTGTCTGCTACAGCTT 999
QY 776 CATCATT 782
Db 1000 CATGATT 1006

RESULT 14
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
; US-08-454-549-1

Query Match 3.6%; Score 59.8; DB 2; Length 2706;
Best Local Similarity 45.6%; Pred. No. 2.2e-07;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

QY 235 GCGCTTCACTTCAATGCTTATTTGGCGGCTGGTGGG---TGTGATTTCCATTTCTTCC 291
Db 264 GGGCTTCACTTGGCTGTGTGCAATCGGGGGCTCTCTGGGAACTGCTGTGATGATGCA 323
QY 292 TCTGTGTAATAATGACACCGGTCAGTGAACACCATGGCGGTCAATTAATGTTGGTGG 351
Db 324 TCTCAGGACACCAAGATGAAGACAGTACCAATTTACATTTAATGTGGCACTGG 383

QY 352 TCACAGCGTTTCTGTGTGACAGTGCATTTGCTTGACTTACTATCAAGAAGACTT 411
Db 384 CTGATACCCCTGGTGTGTCTAACTGTCCTTCCAGGGCAGACATCTTACTGGGCTTCT 443
QY 412 GGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATGCTGCAATCCACATGATGAC 471
Db 444 GGGCATTTGGGAATGCACTCTGCAAGACTGTGATGCTATGATGACTTACAAACATGTTA 503
QY 472 TCAGCTTCATTTCTATGTGTGATCTGTGTACACAGATACCTGATCTTCTTCAAGTCA 531
Db 504 CCAGACATTTACTCTGACCGCCCATGAGCGGTAACCGGTATGTGGTATCTGCCACCTTA 563
QY 532 AAGACAAAGTGAATTTCAAGAAAATCGACTGTGTGCTGCCAGTGTGGCATGTGGA 591
Db 564 TCCGTGCCCTTGAATGTGAGCATCCAGCAAAAGCCAGGCTGTAAATGTGGCCATATGAGG 623
QY 592 CGCTGTGATTTGTATTTGTGGTACCCCGTGTGCTCCCGGTATGATCATGAGGAAT 651
Db 624 CCTGGCTTCAGTGTGTGTGTCTGTGTGTCATATGAGTTTCAGCAACAGTGAAGATG 683
QY 652 ACAATGAGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAATAATCA 711
Db 684 AAGAGATGAGTGTCTGTGTGAATCCCTGCCCTCAGAGACTATTTGGGGCCCTGTATTGG 743
QY 712 TCAACTATATGATGATGATTTTGTCAATAGCCGTGCTGTGATTTCTGTGCTTCCAGG 771
Db 744 CCATCTGCATCTTCTTCTTTTCTTCTTCAATCATCCCTGTGTGATCATCTGTCTGTACA 803
QY 772 TCTTCATCATT 782
Db 804 GCTCATGATT 814

RESULT 15
US-08-454-552-1
; Sequence 1, Application US/08454552
; Patent No. 6005072
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,552
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 01:56:38 ; Search time 6088.21 Seconds
(without alignments)
10528.586 Million cell updates/sec

Title: US-10-085-233B-1

Perfect score: 1684
Sequence: 1 tcgcacagtcgacacattt.....cttcatgcagtcgacgscg 1684

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	644.4	38.3	694	9	AG145972
3	642.2	38.1	717	7	CO918845
4	415.8	24.7	772	2	BF160725
5	354.2	21.0	580	8	AZ554824
6	338	20.1	456	8	AQ888495
7	325.8	19.3	678	5	BX952455
8	280.6	16.7	306	7	CV329473
9	237.2	14.1	646	4	BG862323
10	203	12.1	499	6	CD699779
11	199	11.8	478	4	BG145683
12	181	10.7	649	4	BG461295
13	162	9.6	283	4	BG221739
14	146.2	8.7	2774	3	AK041317
15	142	8.4	834	1	AJ455645
16	111	6.6	680	6	CA355790
17	104	6.2	643	7	CF906536
18	104	6.2	644	7	CF906232
19	103.6	6.2	598	7	CF905741
20	90.6	5.4	529	5	BU698671
21	86.4	5.1	661	6	BY748361
22	82	4.9	705	6	CN793065
23	76.2	4.5	679	6	CD469227
24	72.2	4.3	733	6	CA050323

25	71.4	4.2	648	6	CB514250	CB514250
26	70	4.2	659	9	B0563030	B0563030
27	70	4.2	996	9	AY401267	AY401267
28	69.8	4.1	879	9	AY410745	AY410745
29	69.4	4.1	866	6	CD246184	CD246184
30	69.4	4.1	980	4	BM543468	BM543468
31	68.6	4.1	542	6	CA965628	CA965628
32	67	4.0	672	7	CO957761	CO957761
33	64.4	3.8	671	5	BY752012	BY752012
34	62.6	3.7	353	5	BY183952	BY183952
35	61.2	3.6	679	6	BY750559	BY750559
36	60.2	3.6	785	4	BI754749	BI754749
37	60	3.6	450	6	CA576592	CA576592
38	60	3.6	607	2	BB634972	BB634972
39	60	3.6	689	6	BY751880	BY751880
40	59.8	3.6	2919	3	AK038620	AK038620
41	59.8	3.6	2959	3	AK079529	AK079529
42	59	3.5	695	6	BY751732	BY751732
43	58	3.4	718	7	CO570572	CO570572
44	58	3.4	791	6	CD559646	CD559646
45	58	3.4	791	6	CD559647	CD559647

ALIGNMENTS

RESULT 1
CO918710
LOCUS
DEFINITION
AGENCOURT 30488597 NIH MGC 145 Homo sapiens CDNA clone
IMAGE:7211820 5', mRNA sequence.
ACCESSION
CO918710
VERSION
CO918710.1 GI:51266406
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 694)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: IRH5 row: c column: 10
High quality sequence stop: 489.
Location/Qualifiers
1. 694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7211820"
/feature_type="mixed"
/lab_host="DH10B"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/NotI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
http://image.llnl.gov/image/rearranged_plates/IRBI_presv.dat

FEATURES

source

ORIGIN a Note: this is a NIH_MGC Library."

Query Match 40.3%; Score 678.8; DB 7; Length 694;
Best Local Similarity 98.6%; Pred. No. 1e-176;
Matches 663; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 157 GTGACTTCCCAAGTATGCTGGGACAAATACCTCCAGAAATTCCTTGCATCTTATAG 216
DB 2 GTGACTTCCCAAGTATGCTGGGACAAATACCTCCAGAAATTCCTTGCATCTTATAG 61
QY 217 TGAACACCCCACTTAATGAGCTTCACTTCAATGCTTAAATGGCGGGCTGGTGGTGA 276
DB 62 TGAACACCCCACTTAATGAGCTTCACTTCAATGCTTAAATGGCGGGCTGGTGGTGA 121
QY 277 TTTTCATCTTTTCCCTCGTGAATGAACACCGGTCAGACACCAATGCGGGTGA 336
DB 122 TTTTCATCTTTTCCCTCGTGAATGAACACCGGTCAGACACCAATGCGGGTGA 181
QY 337 TTAACCTGGTGTGTCAACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTTACC 396
DB 182 TTAACCTGGTGTGTGTCAACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTTACC 241
QY 397 TCAATCAAGAAAGACTTGAATGTTGGGCTGCGCTTCTGCAAAATTTGAGTGCATGTC 456
DB 242 TCAATCAAGAAAGACTTGAATGTTGGGCTGCGCTTCTGCAAAATTTGAGTGCATGTC 301
QY 457 ACATCCAGATGTAACCTGAGTTCCTATCTAATGTTGATGTCGTCACCAATGATCTGA 516
DB 302 ACATCCAGATGTAACCTGAGTTCCTATCTAATGTTGATGTCGTCACCAATGATCTGA 361
QY 517 TCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATGCTAGTGGTGGTGA 576
DB 362 TCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATGCTAGTGGTGGTGA 421
QY 577 GTGCTGGCATGTGAGCGTGTGATTTGCAATGTGTGATCCCTGTTGTCCTCCGGTATG 636
DB 422 GTGCTGGCATGTGAGCGTGTGATTTGCAATGTGTGATCCCTGTTGTCCTCCGGTATG 481
QY 637 GAATCCAGATGTAACCTGAGTTCCTATCTAATGTTGATGTCGTCACCAATGATCTGA 696
DB 482 GAATCCAGATGTAACCTGAGTTCCTATCTAATGTTGATGTCGTCACCAATGATCTGA 541
QY 697 CATATGTAAGAAATCATCAATATATGATGATGATTTTGTGATGAGCGTGTGATGTC 756
DB 542 CATATGTAAGAAATCATCAATATATGATGATGATTTTGTGATGAGCGTGTGATGTC 601
QY 757 TGTGTGCTTCCAGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 816
DB 602 TGTGTGCTTCCAGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 817 TATCCACAGAGGATGCTGGGCTCAGCTGAAAA 849
DB 662 TATCCACAGAGGATGCTGGGCTCAGCTGAAAA 694

RESULT 2
AG145972 684 bp DNA linear GSS 08-JUN-2002
LOCUS AG145972
DEFINITION Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey
sequence.
ACCESSION AG145972
VERSION AG145972.1 GI:16675650
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library RPCI-43
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 684)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsunuma-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanse@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..684
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-007G22.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 38.3%; Score 644.4; DB 9; Length 684;
Best Local Similarity 98.2%; Pred. No. 3.7e-167;
Matches 662; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 531 AAAAGCAAGTGAATTTCTACAGAAATGCTGATGCTGCTGCAAGTCTGGATGTGG 590
DB 10 AAAAGCAAGTGAATTTCTACAGAAATGCTGATGCTGCTGCAAGTCTGGATGTGG 69
QY 591 AGCGTGTGATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 650
DB 70 AGCGTGTGATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 129
QY 651 TACAAATGAGAGCACTGTTTAAATTTCAAAAGCTTGTCTTACACATATGTAATTC 710
DB 130 TACAAATGAGAGCACTGTTTAAATTTCAAAAGCTTGTCTTACACATATGTAATTC 189
QY 711 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
DB 190 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
QY 771 GTCTTCATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 830
DB 250 GTCTTCATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
QY 831 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTATCCTTGTGTTCTTCC 890
DB 310 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTATCCTTGTGTTCTTCC 369
QY 891 TACAGATTTTATAGATCTATTTATGATGATGATGATGATGATGATGATGATGATGAT 950
DB 370 TACAGATTTTATAGATCTATTTATGATGATGATGATGATGATGATGATGATGATGAT 429
QY 951 AAGGTGATTTTATAGAAATCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1010
DB 430 AAGGTGATTTTATAGAAATCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 489
QY 1011 CTTCCTTTTGTCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATATTTGCTTATGAT 1070
DB 490 CTTCCTTTTGTCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATATTTGCTTATGAT 549
QY 1071 TGTGTTTGTGCGCTTGAAGCAAAATGATGATGATGATGATGATGATGATGATGATGAT 1130
DB 550 TGTGTTTGTGCGCTTGAAGCAAAATGATGATGATGATGATGATGATGATGATGATGAT 609

QY 1131 AT-AAAATGGGTATAGGGAGTAAAGATGTTATTTCTTACTTATGATCAAAACCATCCT 1189
| | | | |
Db 610 ATAAAATGGGTATAGGGAGTAAAGATGTTATTTCTTACTTATGATCAAAACCATCCT 669
| | | | |
QY 1190 TGATGTACCCAAA 1203
| | | | |
Db 670 TGATGTACCCAAA 683
| | | | |
RESULT 3
CO18845/c 717 bp mRNA linear EST 16-AUG-2004
LOCUS AGENCOURT 30698387 NIH MGC 145 Homo sapiens cDNA clone
DEFINITION IMAGE:7211820 3', mRNA sequence.
ACCESSION CO18845
VERSION CO18845.1 GI:51266673
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 717)
NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: IRBIS row: c column: 10
High quality sequence stop: 515.
Location/Qualifiers
1. 717
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7211820"
/issue_type="mixed"
/lab_host="DH10B"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBIS-presv.dat
a Note: this is a NIH-MGC Library."

ORIGIN
Query Match 38.1%; Score 642.2; DB 7; Length 717;
Best Local Similarity 98.4%; Pred. No. 1.5e-166;
Matches 656; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 483 TTTATGTGTGATCTGTACCAAGTATCTATCTTCTCAAGTCAAAAGCAAGT 542
| | | | |
Db 669 TTTATGTGTGATCTGTACCAAGTATCTATCTTCTCAAGTCAAAAGCAAGT 610
| | | | |
QY 543 GAATTCACGAAAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
| | | | |
Db 609 GAATTCACGAAAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
| | | | |
QY 603 GTCAATGTGTACCCCTGTTGTCTCCGGTATGGAATCATGAGAAATCATGAGAG 662
| | | | |

Db 549 GTCAATGTGTACCCCTGTTGTCTCCGGTATGGAATCATGAGAAATCATGAGAG 490
| | | | |
QY 663 CATCTTTTAAATTTTCAAAAGCTTGTCTTATACATATGTGAAATCATCATATATG 722
| | | | |
Db 489 CACTGTTTAAATTTTCAAAAGCTTGTCTTATACATATGTGAAATCATCATATATG 430
| | | | |
QY 723 ATAGTATTTTTCATAGCCGTTGCTGATCTGTGTGCTTCCAGGCTTCATCATTT 782
| | | | |
Db 429 ATAGTATTTTTCATAGCCGTTGCTGATCTGTGTGCTTCCAGGCTTCATCATTT 370
| | | | |
QY 783 ATGTTATGTGTGAGAGAGTACGCCACTCTTATCTATCCACAGAGTTCTGGGCTCAG 842
| | | | |
Db 369 ATGTTATGTGTGAGAGAGTACGCCACTCTTATCTATCCACAGAGTTCTGGGCTCAG 310
| | | | |
QY 843 CTGAAAACCTATTTTATAGGGGTCACTCTGTTGTTCTTCCCTACAGTTCTTT 902
| | | | |
Db 309 CTGAAAACCTATTTTATAGGGGTCACTCTGTTGTTCTTCCCTACAGTTCTTT 250
| | | | |
QY 903 AGGATCTATTACTGTAATGTGTGAGCAATTCGAATGCCGTGACAGAGTTGCATTT 962
| | | | |
Db 249 AGGATCTATTACTGTAATGTGTGAGCAATTCGAATGCCGTGACAGAGTTGCATTT 190
| | | | |
QY 963 TATAAGAAATCTTCTTGAAGTGAAGCAAGCAATAGCTGATGATTTGCTTCTTGTTC 1022
| | | | |
Db 189 TATAAGAAATCTTCTTGAAGTGAAGCAAGCAATAGCTGATGATTTGCTTCTTGTTC 130
| | | | |
QY 1023 TTTGGGGGAAGCCATGTTTAAAGCAAAAGATATAGCTTATGAAATGTGTTTGTGC 1082
| | | | |
Db 129 TTTGGGGGAAGCCATGTTTAAAGCAAAAGATATAGCTTATGAAATGTGTTTGTGC 70
| | | | |
QY 1083 CGTTACCCCAAACTACATATTCATATTTGCTTCTTATATTTGGAAAT-AAAAGGGT 1141
| | | | |
Db 69 CGTTACCCCAAACTACATATTCATATTTGCTTCTTATATTTGGAAAT-AAAAGGGT 10
| | | | |
QY 1142 ATAGGGGAG 1150
| | | | |
Db 9 ATAGGGGAG 1
| | | | |

RESULT 4
BF160725 772 bp mRNA linear EST 30-OCT-2000
LOCUS 601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',
DEFINITION mRNA sequence.
ACCESSION BF160725
VERSION BF160725.1 GI:11040832
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 772)
NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LHAM9196 row: f column: 07
High quality sequence stop: 634.
Location/Qualifiers
1. 772
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3988230"

/issue_type="spontaneous tumor, metastatic to mammary.
 Stem cell origin."
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;
 Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 24.7%; Score 415.8; DB 2; Length 772;
 Best Local Similarity 79.2%; Pred. No. 1.1e-103;
 Matches 544; Conservative 0; Mismatches 137; Indels 6; Gaps 4;

261 GGGCTGCTGGGTGCTATTTTCATCTTTCTCCCTGCTGAAAAATGAACCCGGTAGTG 320
 1 GGACTGTAAGGCTCATCTTCATCTCTGTTCTGCTGTAATAATGAACCTCAAGTGA 60
 321 ACCACCATGCGCTCATTAATCTGTGTGTCACAGCGTTTCTGCTGACAGTGC 380
 61 ACCACCATGCTGTCTATCAACCTGTGTGTTCATGAGGCTCTTCTACTGACGTCCT 120
 381 TTTCGCTTGACTCACTCATCAAGAAAGACTTGATGTTGGCTGCTCTTCTGCAATTT 440
 121 TTCCGCTTGGCACTCACTCAAGGAGACTTGACG-TTGAATTACCTTCTGCAATTT 179
 441 GTGAGTGCATGCTGACATCCACATGTAACCTGACCTTCTTCTATGAGGATCCTG 500
 180 GTGAGTGCATGTAATCAATCAATGATGTAACCTTCTTCTGAGGATCACTA 239
 501 GTCCACGATACCTCATCTTCTTCAAGTGCAGAAAGACAAAGTGAATTTCAAGAAACTG 560
 240 GTCCATGATACCTCATCTTCTTCAAGCGTAGAGCAAAAGTGAATTTCAAGAAACTG 299
 561 CATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
 300 CATGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
 621 GTTGTCTCCCGGATGGAATTCATGAGAAATCAATGAGAGACATGTTTAAATTTGAC 680
 360 GTGCTTCTCAAGTGAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 419
 681 AAAGACTTGTCAATATGTAATATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 740
 420 AAAGACTTGTCAATATGTAATATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 479
 741 GCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
 480 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
 801 CTACGCACTTCTTACTATCCACGAGAGTCTGAGGCTCAGCTGAGAAACCTATTTT 860
 540 TTTCGCACTTCTTACTAT-CCACGAGAGTCTGAGGCTCAGCTGAGAAACCTATTTT 598
 861 ATAGAGGTCA--TCCCTGTTGTTTCTCTTCCCTACAGTCTTTAGATTAATTTG 917
 599 ATAGAGTACATATCAATTTGGGTTTCTTCCCTACAGTCTTTAGATTAATTTG 917
 918 AATGTTGTAAGCATTCATGCTCT 944
 658 TGTGTTGGGGGCTGCCAGAGCTGT 684

RESULT 5
 A2554824 580 bp DNA linear GSS 20-NOV-2000
 LOCUS
 DEFINITION
 RPCI-23-211E13.TV RPCI-23 Mus musculus genomic clone
 ACCESSION
 A2554824
 VERSION
 A2554824.1 GI:11234644
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 580)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatman, S.,
 Akintet, B., Levins, M., McGinn, S., Tsegaye, G., Geer, K., Krol, M., de
 Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other GSSes: RPCI-23-211E13.TV
 CONTACT: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
 Plate: 211 row: E column: 13
 Seq primer: 17
 Class: BAC ends.

FEATURES

source location/Qualifiers
 1..580
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-211E13"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1:
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Site
 selected DNA was cloned into the pBAC3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 21.0%; Score 354.2; DB 8; Length 580;
 Best Local Similarity 78.3%; Pred. No. 1.2e-86;
 Matches 450; Conservative 0; Mismatches 123; Indels 2; Gaps 2;

556 AACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
 1 AATTCATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 59
 616 CCTGTGTGTCTCCCGTATGGAATCCATGAGAAATCAATCAATCAATCAATCAATCAATCAAT 675
 60 CCTGTGTGTGTCTCAGTATGGAATATAGCAAGAAATCAATCAATCAATCAATCAATCAATCAAT 119
 676 TTCAAGAGAGTCTTACACATATGGAATATCAATCAATCAATCAATCAATCAATCAATCAAT 735
 120 TCCATTAAGAACTTGACCAATGATTTGTCGAGATTAATCAATCAATCAATCAATCAATCAAT 179
 736 TCATAGCGTGTGCTGATTTCTGTTGCTTCCAGTCTTCATCAATTAATGTTGATGCTGC 795
 180 TCATAGCTGTGCTGATTTCTGTTGCTTCCAGTCTTCATCAATTAATGTTGATGCTGC 239
 796 AGAGCTACGCACTCTTACTATCCACAGAGATTTGAGGCTCAGCTGAGAAACCTAT 855
 240 GGAAGTTTCGCACTCTTACTATCCACAGAGATTTGAGGCTCAGCTGAGAAACCTAT 299
 856 TTTTATAGGGGTATCTCTGTTGTTCTTCCCTACAGTCTTTAGATTAATTTG 915
 300 TCTTATAGGTATCAATTAATTTGTTTCTTCCCTACAGTCTTTAGATTAATTTG 359
 916 TGAATGTTGACGATTCATGCTGTACAGCAAGTGTGATTTTATACGAATCT 975

Db 360 TGTATGTTGTGGCATTCCAGAGCTGTAAACAAAGTTCATTTTACATGAATCC 419
Qy 976 TCTTGAAGTACAGCAATAGCTGTAATGTTGCTTCTTGTCTTGGGGGAGACC 1035
Db 420 TATTGACACACAGCCATCAGCTGCTGTGATTTGCTTTTGTCTTGGAGAGACC 479
Qy 1036 ATTGCTTAAGCAAGATATTTGGCTTATGGAATGTTTGTGCTTATGACACAA 1095
Db 480 ATTGGGTTTAAAGCAAAAGTGTGCAAGTGAATGCTCTTATGACATTAGCA-AGA 538
Qy 1096 CTACAGTATTCATATTTGCTTCTTATATTTGGA 1130
Db 539 TTACATATTTCTTTCTTCCGTGGGAATTGGA 573

RESULT 6
LOCUS AQ888495
DEFINITION HS_3162_B1_B01_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey sequence.
ACCESSION AQ888495
VERSION AQ888495
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PubMed 1049764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3162 row: D column: 1
Seq primer: M13 Reverse
Clases: BAC ends
High quality sequence stop: 456.
Location/Qualifiers
1. 456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3162 Col=1 Row=D"
/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 20.1%; Score 338; DB 8; Length 456;
Best Local Similarity 97.3%; Pred. No. 3.6e-82;
Matches 364; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
Qy 549 TACAGAAATCGATGCTGTGGCTGCAAGTCTGGCATGTGACGCTGGTGAATTCATT 608
Db 1 TACAGAAATCGATGCTGTGGCTGCAAGTCTGGCATGTGACGCTGGTGAATTCATT 60
Qy 609 GTGGTACCCCTGGTGTCTCCCGTATGGAATCATGAGAAATACATGAGACACTGT 668

Db 61 GTGGTACCCCTGGTGTCTCCCGTATGGAATCATGAGAAATACATGAGACACTGT 120
Qy 669 TTTAATTTCAAAAGAGCTTGTCTTACATATGTGAAAATCATATATGATATGTC 728
Db 121 TTTAAATTTCAAAAGAGCTTGTCTTACATATGTGAAAATCATATATGATATGTC 180
Qy 729 ATTTTGTCAATACCCGCTGTGATTTGTTGCTTCCAGGCTTCATCATATATGTC 788
Db 181 ATTTTGTCAATACCCGCTGTGATTTGTTGCTTCCAGGCTTCATCATATATGTC 240
Qy 789 ATGTCAGAGAGCTAGCCACTTTACTATATCCACAGAGTTCGGGCTAGCTGAAA 848
Db 241 ATGTCAGAGAGCTAGCCACTTTACTATATCCACAGAGTTCGGGCTAGCTGANA 300
Qy 849 AACCTATTTTAAAGAGGATCTCTTGTGTTTCTTCCCTTACAGATTCCTTAAATC 908
Db 301 AAACCTATTTTAAAGAGGATCTCTTGTGTTTCTTCCCTTACAGATTCCTTAAATC 957
Qy 909 TATTACTGAATGT 922
Db 358 TATTACTGAATGT 371

RESULT 7
LOCUS BX952455
DEFINITION DKFZp781N17197_r1 781 (synonym: hicc4) Homo sapiens cDNA clone
ACCESSION BX952455
VERSION BX952455
KEYWORDS BX952455.1 GI:43429371
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 678)
Mamburt,R., Heubner,D., Mewes,H.W., Weill,B., Amid,C., Osanger,A., Robo,G., Han,W., and Wiemann,S.
EST (Mamburt,R., Heubner,D., Mewes,H.W., Weill,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
This is from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
No 31 sequence available.
This clone (DKFZp781N17197) is available at the RZPD in Berlin.
Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp781N17197"
/dev stage="adult"
/lab_host="DH10B"
/clone_1lb="781 (synonym: hicc4)"
/note="Vector: pSport1_Sci; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN
Query Match 19.3%; Score 325.8; DB 5; Length 678;
Best Local Similarity 99.1%; Pred. No. 1e-76;
Matches 347; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 153 AATGTGATTTCCCAAGTATGCTGCGCACAATACCTCCAGAAATTCCTTGCATCT 212
Db 349 AAGAGTGAATTTCCCAAGTATGCTGCGCACAATACCTCCAGAAATTCCTTGCATCT 408

QY 213 ATAGTACACCCCACTTAATACAGCCCTCTCATAGTCTTAATGGCGGCGTGGGT 272
|||||
Db 409 ATAGTACACCCCACTTAATACAGCCCTCTCATAGTCTTAATGGCGGCGTGGGT 468
QY 273 GTCAATTTCCATTTCTTTCTCTCTGTGAAATGACACCCCGTCACTGACCGG 332
|||||
Db 469 GTCAATTTCCATTTCTTTCTCTCTGTGAAATGACACCCCGTCACTGACCGG 528
QY 333 GTCAATTTCCATTTCTTTCTCTCTGTGAAATGACACCCCGTCACTGACCGG 392
|||||
Db 529 GTCAATTTCCATTTCTTTCTCTCTGTGAAATGACACCCCGTCACTGACCGG 588
QY 393 TACCTCATCAGAGAGCTTGATGTTGGGCTGCGCTTCTGCAAAATTTGAGTGCATG 452
Db 589 TACCTCATCAGAGAGCTTGATGTTGGGCTGCGCTTCTGCAAAATTTGAGTGCATG 648
QY 453 CTGCACATCCACATGTAAGTCTGACGTTCCTA 482
|||||
Db 649 CTGCACATCCACATGTAAGTCTGACGTTCCTA 678

RESULT 8
CV329473 306 bp mRNA linear EST 24-SEP-2004
LOCUS CV329473
DEFINITION IL2-UM0076-180500-088-H05 UM0076 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV329473
VERSION CV329473.1 GI:52652687
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias, N.E.R., Garcia Correea, R., Verjovski-Almeida, S., Brlones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers

FEATURES
source 1..306
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="UM0076"
/note="Organ: uterus; Vector: puc18; Site 1: Smal; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORFESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 16.7%; Score 280.6; DB 7; Length 306;
Best Local Similarity 98.0%; Pred. No. 2.7e-66;
Matches 294; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1285 CCAAGTGTGTAATCCACCTGAGTTGCAATATTACATTAATTTCCAGTACAGATGTC 1344
|||||
Db 8 CCAAGTGTGTAATCCACCTGAGTTGCAATATTACATTAATTTCCAGTACAGATGTC 67
QY 1345 TGTGTGCCCCATGAAAGCAACATAGATTTTAAAGATTTTAAAGATTTTAAAGATTTT 1404
|||||
Db 68 TGTGTGCCCCATGAAAGCAACATAGATTTTAAAGATTTTAAAGATTTTAAAGATTTT 126
QY 1405 TAAAGTTCCTCTGTTGAAGCATGCTCTCTAGTCTTTTGAAGTCTGAACTGAGACCTTTAGTT 1464
|||||
Db 127 TAAAGTTCCTCTGTTGAAGCATGCTCTCTAGTCTTTTGAAGTCTGAACTGAGACCTTTAGTT 186
QY 1465 CTTTTCATCCCACTTCCACATAGTAAGTAATTTGCGCCACACCCAGCTCAAGACA 1524
|||||
Db 187 CTTTTCATCCCACTTCCACATAGTAAGTAATTTGCGCCACACCCAGCTCAAGACA 246
QY 1525 CAAACTCTCTCTGCTTAAACAGGTTAGATGTCCTCATCTCATGCTGCTGATAAAACT 1584
|||||
Db 247 CAAACTCTCTCTGCTTAAACAGGTTAGATGTCCTCATCTCATGCTGCTGATAAAACT 306

RESULT 9
BG862323 646 bp mRNA linear EST 29-MAY-2001
LOCUS BG862323
DEFINITION 602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
mRNA sequence.
ACCESSION BG862323
VERSION BG862323.1 GI:14212861
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Purth
Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10828 row: b column: 01
High quality sequence stop: 644.
Location/Qualifiers

FEATURES
source 1..646
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:4917024"
/tissue="IMAGE:4917024"
/dev_stage="tumor, gross tissue"
/lab_host="DH10B"
/clone_id="NCI CGAP Mam4"
/note="Organ: mammary; Vector: PCMV-SPORE6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Purth,
NIH Reference for transgenic model: Yi et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 14.1%; Score 237.2; DB 4; Length 646;
Best Local Similarity 79.4%; Pred. No. 3.8e-54;
Matches 281; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

OY		157	GTGACTTCCCAAGTATGCTGGCGACAATAACGCCAAGAATTCCCTTGCCATTCCTATAG	216
Db		293	GTAATGTTTGAAGAATGATGATATATAAACCCTGAGAAATTCCTTGTGACCTATPAC	352
OY		217	TGACACCCCACCTTAATACAGCCTCTACCTTCATAGTGCCTTATTTGGCGGGCTGTGGGTGCA	276
Db		353	TGGCACACACACTTAACATGATTTTACTCATATGCTCTCATTTGGAGAACCTGTGAGCCCTCA	412
OY		277	TTTTCAATCTTTTTCCTCCTGTGTGAATAAGACACCCGGTCAGTGAACCAACCATGGGGGTCA	336
Db		413	TCTCCATCCGGTCTTCTGTGGTGGAATAATGAACCTCAACGTTTCAAGTAGCAACCATGGCTGCA	472
OY		337	TTAACTGTGTGTGTGCCACAGCGTCTTTCCTGTGACAGTGCATTTTGGCTTGACTTAC	396
Db		473	TCAACCTGTGTGTGTTCATGGGGTCTTCTCACTACAGGTGCTTTCGGCTTGGGATAC	532
OY		397	TCATCAAGAAAGACTTGATGTTTGGGGCTGCCCTTCTGCMAATTTTNGAGTGCATGAC	456
Db		533	TCATCAAAGGAGCTTGGAGCGTTTGATTAACCTTCTGCMAATTTTNGAGTGCATGATAC	592
OY		457	ACATCAACATGACTTCAACGTTCTTAATCTATGTGTGATTCCTGTGACCAAGAT	510
Db		593	ATATCAACATGATCACTCAACGTTCTCTTCTTACGTGTGATGATGATCATGAT	646
RESULT	10			
	CD699779	499 bp	mRNA	linear EST 25-JUN-2003
LOCUS	EST16303		human nasopharynx Homo sapiens cDNA, mRNA sequence.	
DEFINITION	CD699779			
ACCESSION	CD699779.1	GI:32229387		
VERSION	EST.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 499)			
AUTHORS	Liu,X.-Q., Zhou,Y., Zhang,J.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel.: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@zsune.edu.cn. Location/Qualifiers			
FEATURES				
source	1..499			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/issue_type="normal nasopharynx"			
	/clone_lib="human nasopharynx"			
	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
Query Match	12.1%; Score 203; DB 6; Length 499;			
Beech Local Similarity	100.0%; Pred. No. 1.le-44;			
Matches	203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	157	GTGACTTCCCAAGTATGCTGGCGACAATAACGCCAAGAATTCCCTTGCCATTCCTATAG	216	
Db	297	GTGACTTCCCAAGTATGCTGGCGACAATAACGCCAAGAATTCCCTTGCCATTCCTATAG	356	
OY	217	TGACACCCCACCTTAATACAGCCTCTACCTTCATAGTGCCTTATTTGGCGGGCTGTGGGTGCA	276	
Db	357	TGACACCCCACCTTAATACAGCCTCTACCTTCATAGTGCCTTATTTGGCGGGCTGTGGGTGCA	416	
OY	277	TTTTCAATCTTTTCTCCTGTGTGAATAAGACACCCGGTCAGTGAACCAACCATGGGGGTCA	336	

Db	417	TTTCATTCTTTCTCTCTGGTGAATAAGACACCCGGTCAGTACACACATGCGGCTCA	476
Qy	337	TTAACTTGSTGTGTGTCCACAGC	359
Db	477	TTAACTTGSTGTGTGTCCACAGC	499
RESULT 11			
BGI45683		478 bp	linear
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
COMMENT			
FEATURES			
source			

Db 180 GGTAAAGCAAAAGATTGACATGTCGAAATGCTCTTATGCAATTAAGCA-AGATTAC 238
QY 1100 AGTATTCATATTGTTCTTCCCTTATATTTGGGAATTAAGGATPAGGAGGTAAGANG 1159
Db 239 CATATTCCTTTCTTCTCTGTTGGGAATTTGGAATACGA-----AGAGCTTAAGAAATG 289
QY 1160 GATATTCATATTGTTGATCAAAACCATGCTGTATGATACCAAAAGAAAGCTATTA 1219
Db 290 ATTTTCATGCTTCAATGAAACCTGCGCTTGCCCAACC-AAACAAAGGAATTAAGAG 348
QY 1220 TGGAAAGCCCTCATGTTAGTCTCTTATGGATATCCCTCCATCTCTAGAGATGCGCTAC 1279
Db 349 TGTCCAAAGCTCTTACTACGCGCTGATAAATACTGTGTGTGGGA-AGGTGTCATATC 407
QY 1280 AAAGACAGTGTGTTGAATTCACCTGAGTTGCAATTAATTAATTTTCCAGTACAGA 1339
Db 408 AAAGATGATGTGTAGAGAACTATACGGAATTCGTATTCATTTTTCACATAC 467
QY 1340 ATGCTGTGTGT 1350
Db 468 GTGTCTACTTG 478

RESULT 12
Bg461295 649 bp mRNA linear EST 21-APR-2001
LOCUS RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION Bg461295
ACCESSION Bg461295
VERSION Bg461295.1 GI:13749801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 649)
Harrington,J.V., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL
MEDLINE
PUBMED
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com.
Location/Qualifiers
FEATURES
source
1..649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HT1080"
/note=See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 10.7%; Score 181; DB 4; Length 649;
Best Local Similarity 74.1%; Pred. No. 1.5e-38;
Matches 355; Conservative 0; Mismatches 50; Indels 74; Gaps 7;
QY 157 GTGACTTCCCAAGATAGCTGCGCCACAAATACCTCCAGGAATTCCTTGGCATCTTAG 216
Db 108 GTGACTTCCCAAGATAGCTGCGCCACAAATAC-----TCTTATCTTATAG 151

QY 217 TGACACCCCACTTAATACAGCCTCTACTTCATAGTCTTATTGGCGGGCTGTGGTCA 276
Db 152 TGACACCCCACTTAATACAGCCTCTACTTCATAGACTTATTGGCGGCTGAGAGGTGCA 211
QY 277 TTTGCATTTCTTTCTCTCTGTTGAAAATGAACACCCGGTCAGTGAACCAATGCGGTCA 336
Db 212 TTTGCATTTCTTTCTCT-----CCGGTCAGTGACCAATGCGGTCA 254
QY 337 TTAATGTTGTGTGTGCAAGCGTTTCTGTGTCAGAGTGC-CAATTCGTGTGACCTAC 395
Db 255 TTAATGTTGTGTGTGTCAGAGCGTTATCTGTGTCAGTGC-CAATTCGTGTGACCTAC 314
QY 336 CTCATCAAGAAAGATGTGATGTTGGGCTGCGCTTCTGCAATTTGTGAGTGCATGCTG 455
Db 315 C-----CTTTGGGCTGCGCTTCTGCAATATGATGATGATGATGCTG 356
QY 456 CACATCCACATGATACCTGACGTTCTT-ATTATATGTGTATCTGTGTCACCAATACCT 514
Db 357 AACATTCACATGATACCTGACGATCCTTAATTCATGCGGTGATCCTGCGCGCGGAT 412
QY 515 CATCTTCTTCAAGTCAAGCAAGATGGAATTCACGAAACATGATGCTGTGCTGC 574
Db 413 -----CAAGACAAAGCGACTT-TACAGATGCTGCGCCCGAGGTTGC 455
QY 575 CAGTCTGCGCATGTGAGAGCTGTGATTTGTCAATTTGTGTACCCCTGTTGTTCCCGGT 633
Db 456 CAGACTGCGCATGTGAGAGCCTGTTGATTTGATGTCGCGGCGCCCGCGGTTCGGGT 514

RESULT 13
Bg221739 283 bp mRNA linear EST 21-APR-2001
LOCUS RST41554 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION Bg221739
ACCESSION Bg221739
VERSION Bg221739.1 GI:13747760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 283)
Harrington,J.V., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL
MEDLINE
PUBMED
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 233.
Location/Qualifiers
FEATURES
source
1..283
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HT1080"
/note=See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match	9.6%; Score 162; DB 4; Length 283;
Best Local Similarity	100.0%; Pred. No. 2.2e-33;
Matches 162; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	157 GTGACCTCCAGATGATGCTGGCCACATACCTCCAGGAATTCCTTGGCATCTTAG 216
Qy	122 GTGACCTCCAGATGATGCTGGCCACATACCTCCAGGAATTCCTTGGCATCTTAG 181
Db	217 TGACACCCCACTTATGAGCTCTTACCTTATGCTTATTTGGCGGCTGGTGGTCTCA 276
Qy	182 TGACACCCCACTTATGAGCTCTTACCTTATGCTTATTTGGCGGCTGGTGGTCTCA 241
Db	277 TTTCATTTCTTCTCTCTGTTGAATGAAACACCCGCTAG 318
Qy	242 TTTCATTTCTTCTCTCTGTTGAATGAAACACCCGCTAG 283
RESULT 14	
AK041317	2774 bp mRNA linear HTC 03-APR-2004
LOCUS	
DEFINITION	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530099J19 product:hypothetical Rodopsin-like GPCR superfamily containing protein, full insert sequence.
ACCESSION	AK041317
VERSION	AK041317.1 GI:26334372
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	99279253
MEDLINE	10349636
PUBMED	
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	20499374
MEDLINE	11042159
PUBMED	
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishii, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Watanabe, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL	20530913
MEDLINE	11076861
PUBMED	
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
JOURNAL	5
MEDLINE	
PUBMED	
REFERENCE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL	6 (bases 1 to 2774)
MEDLINE	
PUBMED	
REFERENCE	6 Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

TITLE	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Direct Submission
COMMENT	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
FEATURES	cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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QY 487 ATGTGGTGAATCTGTGTCACAGATACCTCATCTTTCTTCAAGTGCAGAACAAAGTGAAT 546
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Db 720 AGTTACAAAAGTTCATGCGCGTGTCTAAGTATTTATTTGGGAGCAGGAAGCTTCA 779
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RESULT 15
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DEFINITION AJ455645
ACCESSION AJ455645
VERSION AJ455645.1 GI:20265741
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 834)
Buerstedde, J.M.
Gallus gallus bursa lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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ORIGIN

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Matches 225; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

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Db 438 CCTGATTTACTGTCTACTAGTTGCCCTTTGCTGGAGAGTGGATAGGATCACTGCANATGC 497
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QY 287 TTTCCTCTGTGAAATGAAACACCCGGTCAAGTACACCATGCGGTTCATTACTTGGT 346
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Search completed: September 10, 2005, 09:59:38
Job time : 6093.21 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:41:45 ; Search time 1214.69 Seconds
(without alignments)
9104.583 Million cell updates/sec

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Perfect score: 1684
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 731250 seqs, 3283620254 residues
Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1472.6	87.4	2525	21	US-10-975-979-81
5	1472.2	87.4	113306	17	US-10-292-798-1007
6	1228.6	73.0	1336	19	US-10-467-252-52
7	1118.8	66.4	1318	15	US-10-017-161-1193

8	1106.2	65.7	1340	19	US-10-467-252-53	Sequence 53, Appl1
9	1106.2	65.7	1460	19	US-10-467-252-54	Sequence 54, Appl1
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11	968	57.5	1040	15	US-10-293-171-1	Sequence 1, Appl1
12	939	55.8	939	14	US-10-085-233B-3	Sequence 3, Appl1
13	916.4	54.4	918	9	US-09-995-225-3	Sequence 3, Appl1
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15	916.4	54.4	918	14	US-10-055-106C-1	Sequence 1, Appl1
16	916.4	54.4	918	14	US-10-188-405-9	Sequence 9, Appl1
17	916.4	54.4	918	17	US-10-297-908A-2	Sequence 2, Appl1
18	913.4	54.2	1632	21	US-10-505-486-212	Sequence 212, App
19	559.2	33.2	810	16	US-10-366-504-1	Sequence 1, Appl1
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23	83.6	5.0	600	22	US-10-972-079-57479	Sequence 57479, A
24	76.4	4.5	1113	10	US-09-826-509-540	Sequence 540, App
25	76.4	4.5	1113	21	US-10-925-095-540	Sequence 540, App
26	76.4	4.5	1805	9	US-09-823-114-18	Sequence 18, Appl1
27	76.4	4.5	1805	15	US-10-290-748-18	Sequence 18, Appl1
28	76.4	4.5	1829	10	US-09-905-186A-9	Sequence 9, Appl1
29	76.4	4.5	1829	10	US-09-905-186A-10	Sequence 10, Appl1
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32	76.4	4.5	1973	18	US-10-641-643-1417	Sequence 1417, Ap
33	76.4	4.5	1973	22	US-10-498-848-1	Sequence 1, Appl1
34	76.4	4.5	2534	14	US-10-087-345A-22	Sequence 22, Appl1
35	76.4	4.5	2534	15	US-10-825-667A-208	Sequence 208, Appl
36	76.4	4.5	2534	17	US-10-352-684A-31	Sequence 31, Appl1
37	76.4	4.5	2534	21	US-10-753-267-77	Sequence 77, Appl1
38	76.4	4.5	2534	22	US-10-848-637-72	Sequence 22, Appl1
39	76.4	4.5	2534	24	US-11-011-450-22	Sequence 22, Appl1
40	76.4	4.5	3330	20	US-10-723-860-7345	Sequence 7345, Ap
41	74.8	4.4	1829	10	US-09-905-186A-7	Sequence 7, Appl1
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43	73.2	4.3	1134	19	US-10-606-592-14	Sequence 14, Ap
44	71.6	4.3	110218	13	US-10-087-192-1145	Sequence 1345, Ap
45	70.4	4.2	593	16	US-10-029-386-9800	Sequence 9800, Ap

ALIGNMENTS

RESULT 1
US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLICKSMAN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; FILE REFERENCE: RECEPTOR AND USBS THEREFOR
; CURRENT APPLICATION NUMBER: US/10/085,233B
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147) ... (1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Query Match 99.9%; Score 1683; DB 14; Length 1684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1321 CATTAATTTTCCAGTACAGATGCTGTGTGAGCCCATGAAAGCAACATAGGTTTAAAGAT 1380
Db 1321 CATTAATTTTCCAGTACAGATGCTGTGTGAGCCCATGAAAGCAACATAGGTTTAAAGAT 1380
QY 1381 TTTNAGATTTCATTAAGTCTATTAAGTCTCTGTTTGAAGCATGCTCTAGGTTT 1440
Db 1381 TTTNAGATTTCATTAAGTCTATTAAGTCTCTGTTTGAAGCATGCTCTAGGTTT 1440
QY 1441 TGAATGAACTCAGACCTTTAGTTCTTTTCAATCCCACTTCAACCATAGTAAATTTCT 1500
Db 1441 TGAATGAACTCAGACCTTTAGTTCTTTTCAATCCCACTTCAACCATAGTAAATTTCT 1500
QY 1501 GGCACACACCCAGCTCCAAAGACAAACCTCTCTGCTTACAGAGTTAGATGCCAT 1560
Db 1501 GGCACACACCCAGCTCCAAAGACAAACCTCTCTGCTTACAGAGTTAGATGCCAT 1560
QY 1561 TCATCTCATGCTGCTGATTAATACTGATTAAGGGAGGAATAGTAAATTTTCTAGGG 1620
Db 1561 TCATCTCATGCTGCTGATTAATACTGATTAAGGGAGGAATAGTAAATTTTCTAGGG 1620
QY 1621 TATCATTAATCTGTGTAAGAGTATCTGTCTAGACTGAGCAAGCTTATGATGATGCG 1680
Db 1621 TATCATTAATCTGTGTAAGAGTATCTGTCTAGACTGAGCAAGCTTATGATGATGCG 1680
QY 1681 GCCG 1684
Db 1681 GCCG 1684
RESULT 2
US-09-782-974C-81
; Sequence 81, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 2525
TYPE: DNA
ORGANISM: Homo sapiens
US-09-782-974C-81

Query Match 87.4%; Score 1472.6; DB 10; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 153 AATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGGAATTCCTTGGCATCT 212
DB 9 AAGGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGGAATTCCTTGGCATCT 68
QY 213 ATAGTGAACCCCACTTATATAGCTTCACTTATATGCTTATTTGGCGGCTGGTGGT 272
DB 69 ATAGTGAACCCCACTTATATAGCTTCACTTATATGCTTATTTGGCGGCTGGTGGT 128
QY 273 GTCAATTCATCTTTCTCTCTCTGTAAGAAACACCCGCTGATGACCAACCATGGCG 332
DB 129 GTCAATTCATCTTTCTCTCTCTGTAAGAAACACCCGCTGATGACCAACCATGGCG 188
QY 333 GTCAATTCATCTTTCTCTCTCTGTAAGAAACACCCGCTGATGACCAACCATGGCG 392
DB 189 GTCAATTCATCTTTCTCTCTCTGTAAGAAACACCCGCTGATGACCAACCATGGCG 248
QY 393 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGCTTCTGCAATTTTGTAGTGCATG 452
DB 249 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGCTTCTGCAATTTTGTAGTGCATG 308
QY 453 CTGCAACATCCCACTTATATAGCTTCACTTATATGCTTATTTGGCGGCTGGTGGT 512
DB 309 CTGCAACATCCCACTTATATAGCTTCACTTATATGCTTATTTGGCGGCTGGTGGT 368
QY 513 CTCAATCTCTTCAAGTGAAGAAACAAAGTGAATTTCTACAGAAACCTGATGCTGCT 572
DB 369 CTCAATCTCTTCAAGTGAAGAAACAAAGTGAATTTCTACAGAAACCTGATGCTGCT 428
QY 573 GCCAGTGTGATGATGAGCGCTGGTATGCTATGTTGTAACCCCTGTTGTCTCCGG 632
DB 429 GCCAGTGTGATGATGAGCGCTGGTATGCTATGTTGTAACCCCTGTTGTCTCCGG 488
QY 633 TATGAATCCCATGAGGAATATAGTGAAGAGCACTGTTTAAATTTCAAAAGAGCTTGT 692
DB 489 TATGAATCCCATGAGGAATATAGTGAAGAGCACTGTTTAAATTTCAAAAGAGCTTGT 548
QY 693 TACACATATGGAATATCATCACTATATGATGATTTTGTATGATGAGCGGCTGCTG 752
DB 549 TACACATATGGAATATCATCACTATATGATGATTTTGTATGATGAGCGGCTGCTG 608
QY 753 ATTCGTGTGCTTCCAGGCTTCAATCATATATGTTGATGAGTGAAGAGCTGACACT 812
DB 609 ATTCGTGTGCTTCCAGGCTTCAATCATATATGTTGATGAGTGAAGAGCTGACACT 668
QY 813 TTACTATCCCAACGAGAGTCTGGGCTGAGCTGAAAAACCTATTTTATATGGGGCTATC 872
DB 669 TTACTATCCCAACGAGAGTCTGGGCTGAGCTGAAAAACCTATTTTATATGGGGCTATC 728
QY 873 CTGTGTGTCT 932
DB 729 CTGTGTGTCT 788
QY 933 TCCATATGCTTGAAGAGAGGTTGATTTTATATAGAAATCTTCTGATGATGAACGA 992
DB 789 TCCATATGCTTGAAGAGAGGTTGATTTTATATAGAAATCTTCTGATGATGAACGA 848

QY 993 ATTAGCTGCTATGATTTGCTTCTCTTGTCTTTGGGGGAAGCCATGGTTTAAAGAAAG 1052
DB 849 ATTAGCTGCTATGATTTGCTTCTCTTGTCTTTGGGGGAAGCCATGGTTTAAAGAAAG 908
QY 1053 ATTAATGCTTATGGAATTTGTTTGGGCTTGGAGTGAAGCAAACTACATGATATATTT 1112
DB 909 ATTAATGCTTATGGAATTTGTTTGGGCTTGGAGTGAAGCAAACTACATGATATATTT 968
QY 1113 GCTTCCTTATATTTGGGAAT-AAATAGGTAATAGGGAAGTGAAGATGTAATTTCAATTA 1171
DB 969 GCTTCCTTATATTTGGGAAT-AAATAGGTAATAGGGAAGTGAAGATGTAATTTCAATTA 1028
QY 1172 TTGATCAAAACCAAGCTTGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1231
DB 1029 TTGATCAAAACCAAGCTTGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1088
QY 1232 CATTTGATCTTATGGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1291
DB 1089 CATTTGATCTTATGGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1148
QY 1292 TGTGATCAACCTGAGTGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1351
DB 1149 TGTGATCAACCTGAGTGAATTTGTAAGCAAAAGCAAAAGCAAAAGCAAGCTT 1208
QY 1352 CCCATGAAGCAATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1411
DB 1209 CCCATGAAGCAATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1267
QY 1412 CTCTGTTGAAGCAATGCTCTCTGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1471
DB 1268 CTCTGTTGAAGCAATGCTCTCTGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1327
QY 1472 TCCCATCTCAACATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1531
DB 1328 TCCCATCTCAACATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1387
QY 1532 TCCCTGCTCAACATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1591
DB 1388 TCCCTGCTCAACATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1447
QY 1592 GGAAGATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1651
DB 1448 GGAAGATATGATTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGTTTTGAAGT 1507
QY 1652 AGA 1654
DB 1508 AGA 1510

RESULT 3

US-10-467-492A-81
Sequence 81, Application US/10467492A
Publication No. US20050069976A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Vogel, Gabriel
APPLICANT: Land, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: Novel G Protein Coupled Receptor
FILE REFERENCE: 0411PPH0313
CURRENT APPLICATION NUMBER: US/10/467,492A
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.0
SEQ ID NO 81
LENGTH: 2525
TYPE: DNA
ORGANISM: Homo sapiens
US-10-467-492A-81

Query Match 87.4%; Score 1472.6; DB 21; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 153 AAAAGTACTTCCCAAGTATGCTGGGCCAATATCTCCAGGATTTCTCTGGGATCTT 212
| | | | |
Db 9 ACAGGTACTTCCCAAGTATGCTGGGCCAATATCTCCAGGATTTCTCTGGGATCTT 68
| | | | |
QY 213 ATATGACACCCCACTTAATGAGCTCTACTCTATGATGCTTATTTGGCGGGCTGGTGGT 272
| | | | |
Db 69 ATATGACACCCCACTTAATGAGCTCTACTCTATGATGCTTATTTGGCGGGCTGGTGGT 128
| | | | |
QY 273 GTCAATTCATCTTTTCTCTCTGTGAAAAAGAACCCGGTCAAGTACCAACCATGAGCG 332
| | | | |
Db 129 GTCAATTCATCTTTTCTCTCTGTGAAAAAGAACCCGGTCAAGTACCAACCATGAGCG 188
| | | | |
QY 333 GTCAATTCATCTTTTCTCTCTGTGAAAAAGAACCCGGTCAAGTACCAACCATGAGCG 392
| | | | |
Db 189 GTCAATTCATCTTTTCTCTCTGTGAAAAAGAACCCGGTCAAGTACCAACCATGAGCG 248
| | | | |
QY 393 TACCTCATCAAGAGACTTGGATGTTGGGCTGCTCTGCAAAATTTGTGAGTGCATG 452
| | | | |
Db 249 TACCTCATCAAGAGACTTGGATGTTGGGCTGCTCTGCAAAATTTGTGAGTGCATG 308
| | | | |
QY 453 CTGCAATTCATCAAGTATGCTCTGCTCTGATTTATGATGCTGATCTGATCAAGATAC 512
| | | | |
Db 309 CTGCAATTCATCAAGTATGCTCTGCTCTGATTTATGATGCTGATCTGATCAAGATAC 368
| | | | |
QY 513 CTGATCTTCTTCAAGTATGCTCTGCTCTGATTTATGATGCTGATCTGATCAAGATAC 572
| | | | |
Db 369 CTGATCTTCTTCAAGTATGCTCTGCTCTGATTTATGATGCTGATCTGATCAAGATAC 428
| | | | |
QY 573 GCCAGTCTGGCATGCTGAGCGCTGTGATTTGTCAATTTGTGATGCTGATCTGCTCCGG 632
| | | | |
Db 429 GCCAGTCTGGCATGCTGAGCGCTGTGATTTGTCAATTTGTGATGCTGATCTGCTCCGG 488
| | | | |
QY 633 TATGAAATCCATGAGAAATATCAATGAGAGCACTGTTTAAATTTCACAAAAGACTTGT 692
| | | | |
Db 489 TATGAAATCCATGAGAAATATCAATGAGAGCACTGTTTAAATTTCACAAAAGACTTGT 548
| | | | |
QY 693 TACCATATGAGAAATATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 752
| | | | |
Db 549 TACCATATGAGAAATATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 608
| | | | |
QY 753 ATTCTGTTGCTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAAAGCTACGCACTCT 812
| | | | |
Db 609 ATTCTGTTGCTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAAAGCTACGCACTCT 668
| | | | |
QY 813 TTACTATCCACCAAGAGTCTGAGCTGCTGCAAAATCTATTTTATTAAGGGGCTATC 872
| | | | |
Db 669 TTACTATCCACCAAGAGTCTGAGCTGCTGCAAAATCTATTTTATTAAGGGGCTATC 728
| | | | |
QY 873 CTGTTGTTGCTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAAAGCTACGCACT 932
| | | | |
Db 729 CTGTTGTTGCTCTTCCAGTCTTCTATCATTTATGTTGATGCTGAGAAAGCTACGCACT 788
| | | | |
QY 933 TCCATATGCTCTGAGAGAGAGTTCATTTATTAAGAAATCTTCTGAGTGTAAACAGA 992
| | | | |
Db 789 TCCATATGCTCTGAGAGAGAGTTCATTTATTAAGAAATCTTCTGAGTGTAAACAGA 848
| | | | |
QY 993 ATTAGCTGTATGATTTGCTCTTCTGTTGGGGAGAACCATGTTTAAAGCAAAAG 1052
| | | | |
Db 849 ATTAGCTGTATGATTTGCTCTTCTGTTGGGGAGAACCATGTTTAAAGCAAAAG 908
| | | | |
QY 1053 ATTAGTGGCTATGAAATTTGTTTGGCCGTTAGCCAAACATCAAGTATTCATATTT 1112
| | | | |
Db 909 ATTAGTGGCTATGAAATTTGTTTGGCCGTTAGCCAAACATCAAGTATTCATATTT 968
| | | | |
QY 1113 GCTTCTTTATTTATTTGGGAAAT-AAATGGGTTAAGGGGAGTAAAGATGTATTTCAATAC 1171
| | | | |
Db 969 GCTTCTTTATTTATTTGGGAAATAAATGGGTTAAGGGGAGTAAAGATGTATTTCAATAC 1028
| | | | |
QY 1172 TTGATCAAAACCATGCTTGTATGTATCCAAACCAAAAGAGACTATTAATGCAAGACCTT 1231
| | | | |
Db 1029 TTGATCAAAACCATGCTTGTATGTATCCAAACCAAAAGAGACTATTAATGCAAGACCTT 1088
| | | | |

QY 1232 CATTTAGTCTTATGAGGATCCCTCCATCTCTGAGGATGAGCGGTACAAAGACAGTGT 1291
| | | | |
Db 1089 CATTTAGTCTTATGAGGATCCCTCCATCTCTGAGGATGAGCGGTACAAAGACAGTGT 1148
| | | | |
QY 1292 TGTGTAATCCACCTGAGGTTGATTAATTAATTAATTTTCCAGTACAGAAATGTCTGTGG 1351
| | | | |
Db 1149 TGTGTAATCCACCTGAGGTTGATTAATTAATTAATTTTCCAGTACAGAAATGTCTGTGG 1208
| | | | |
QY 1352 CCATGAAAGCAATATGTTTAAAGATTTAAAGATTTAAAGATTTAAAGATTTAAAGATTT 1411
| | | | |
Db 1209 CCATGAAAGCAATATGTTTAAAGATTTAAAGATTTAAAGATTTAAAGATTTAAAGATTT 1267
| | | | |
QY 1412 CTCTGTTGAAGATGCTCTTAAAGTTTGAATGATGATGATGATGATGATGATGATGATGAT 1471
| | | | |
Db 1268 CTCTGTTGAAGATGCTCTTAAAGTTTGAATGATGATGATGATGATGATGATGATGATGAT 1327
| | | | |
QY 1472 TCCCACTTCAACATAGTAATTAATTTCTGAGGATGATGATGATGATGATGATGATGATGAT 1531
| | | | |
Db 1328 TCCCACTTCAACATAGTAATTAATTTCTGAGGATGATGATGATGATGATGATGATGATGAT 1387
| | | | |
QY 1532 TCCCTGCTTCAACAGGTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1591
| | | | |
Db 1388 TCCCTGCTTCAACAGGTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1447
| | | | |
QY 1592 GAGAGAAATGTTAAATTTTCTAGGATGATGATGATGATGATGATGATGATGATGATGAT 1651
| | | | |
Db 1448 GAGAGAAATGTTAAATTTTCTAGGATGATGATGATGATGATGATGATGATGATGATGAT 1507
| | | | |
QY 1652 AGA 1654
| | |
Db 1508 AGA 1510
| | |

RESULT 4
US-10-975-979-81
; Sequence 81, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Schellin, Kathleen
; APPLICANT: Bannigan, Chris
; APPLICANT: Huff, Valerie
; APPLICANT: Kaytes, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Parodi, Luis
; APPLICANT: Hiebsch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PHR293
; CURRENT APPLICATION NUMBER: US/10/975,979
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remainder of Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patent version 3.0
SEQ ID NO 81
LENGTH: 2525
TYPE: DNA
ORGANISM: Homo sapiens
US-10-975-979-81

Query Match 87.4%; Score 1472.6; DB 21; Length 2525;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 153 AAATGACCTTCCCAATGATGCTGGGCAATACCTTCCAGAAATTCCTCTGGGATCT 212
DB 9 ACAGGTGACTTCCCAATGATGCTGGGCAATACCTTCCAGAAATTCCTCTGGGATCT 68
QY 213 ATAGTGACCCCACTTAATCAGCTCTACTTCAATAGCTTAATGGCGGGCTGGTGGT 272
DB 69 ATAGTGACCCCACTTAATCAGCTCTACTTCAATAGCTTAATGGCGGGCTGGTGGT 128
QY 273 GTCAATTCATCTTTCTCTCTGTAAGAAATGAAACCCGGTCAAGTACCAACATGGCG 332
DB 129 GTCAATTCATCTTTCTCTCTGTAAGAAATGAAACCCGGTCAAGTACCAACATGGCG 188
QY 333 GTCAATTCATCTTTCTCTCTGTAAGAAATGAAACCCGGTCAAGTACCAACATGGCG 392
DB 189 GTCAATTCATCTTTCTCTCTGTAAGAAATGAAACCCGGTCAAGTACCAACATGGCG 248
QY 393 TACCTATCAAGAAAGCTTGGATGTTGGGCTGCCCTTCCGAAATTTGGAGTGCATG 452
DB 249 TACCTATCAAGAAAGCTTGGATGTTGGGCTGCCCTTCCGAAATTTGGAGTGCATG 308
QY 453 CTGACATCCCAATGATGCTCAAGTCTCTATTTGATGTTGATGCTGTCACCAATGAC 512
DB 309 CTGACATCCCAATGATGCTCAAGTCTCTATTTGATGTTGATGCTGTCACCAATGAC 368
QY 513 CTGATCTTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATCTGCATGCT 572
DB 369 CTGATCTTTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAATCTGCATGCT 428
QY 573 GCCAGTCTGGCAATGATGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 632
DB 429 GCCAGTCTGGCAATGATGCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 488
QY 633 TATGATCCATGAGGATATCAATGAGAGCACTGTTTAAATTTCAAAAGAGCTTGT 692
DB 489 TATGATCCATGAGGATATCAATGAGAGCACTGTTTAAATTTCAAAAGAGCTTGT 548
QY 693 TACACATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGAT 752
DB 549 TACACATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGAT 608
QY 753 ATTCTGTGTCTTCCAGGCTTCAATATGATGATGATGATGATGATGATGATGATGAT 812
DB 609 ATTCTGTGTCTTCCAGGCTTCAATATGATGATGATGATGATGATGATGATGATGAT 668
QY 813 TTACTATCCCAAGAGGATGCTGGGCTCAGCTGAAAAACCTATTTTAAATGAGGATC 872
DB 669 TTACTATCCCAAGAGGATGCTGGGCTCAGCTGAAAAACCTATTTTAAATGAGGATC 728
QY 873 CTGTGTGTGTCTTCTCTCTCAAGCTTCTTATGATGATGATGATGATGATGATGAT 932
DB 729 CTGTGTGTGTCTTCTCTCTCAAGCTTCTTATGATGATGATGATGATGATGATGAT 788
QY 933 TCCAAATGCTGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
DB 789 TCCAAATGCTGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 993 ATTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052

DB 849 ATTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 908
QY 1053 ATTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
DB 909 ATTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
QY 1113 GCTTCCCTTATATGAGGAT-AAAATGGGATGAGGAGGATGAGGATGAGGATGAGGAT 1171
DB 969 GCTTCCCTTATATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1028
QY 1172 TTGATCAAAACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
DB 1029 TTGATCAAAACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1088
QY 1232 CATTTGATGCTTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291
DB 1089 CATTTGATGCTTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1148
QY 1292 TGTGATCAACCTGAGTGGCAATTTATCATATTTTCCAGTACAGAAATGCTGTGTG 1351
DB 1149 TGTGATCAACCTGAGTGGCAATTTATCATATTTTCCAGTACAGAAATGCTGTGTG 1208
QY 1352 CCATGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1411
DB 1209 CCATGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1267
QY 1412 CTCTGTTTGAAGATGCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1471
DB 1268 CTCTGTTTGAAGATGCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1327
QY 1472 TCCCACTTCACTTGAAGTAAATTTCTGGGCAACCAAGCTCCAAAGACCAAACTC 1531
DB 1328 TCCCACTTCACTTGAAGTAAATTTCTGGGCAACCAAGCTCCAAAGACCAAACTC 1387
QY 1532 TCCCTGCTAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1591
DB 1388 TCCCTGCTAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1447
QY 1592 GGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1651
DB 1448 GGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1507
QY 1652 AGA 1654
DB 1508 AGA 1510

RESULT 5
US-10-292-798-1007
Sequence 1007, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIHO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 08435/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1007
LENGTH: 113306
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source

/ LOCATION: (1) .. (113306)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (201) .. (207)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (11526) .. (12452)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (37954) .. (38097)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (98732) .. (98784)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (112891) .. (113306)
US-10-292-798-1007

Query Match 87.4%; Score 1472.2; DB 17; Length 113306;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 155 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 214
DB 11524 AAGTGAATCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11583
QY 215 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 274
DB 11584 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11643
QY 275 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 334
DB 11644 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11703
QY 335 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 394
DB 11704 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11763
QY 395 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 454
DB 11764 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11823
QY 455 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 514
DB 11824 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11883
QY 515 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 574
DB 11884 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 11943
QY 575 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 634
DB 11944 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12003
QY 635 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 694
DB 12004 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12063
QY 695 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 754
DB 12064 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12123
QY 755 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 814
DB 12124 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12183
QY 815 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 874
DB 12184 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12243
QY 875 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 934
DB 12244 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12303

QY 935 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 994
DB 12304 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12363
QY 995 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1054
DB 12364 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12423
QY 1055 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1114
DB 12424 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12483
QY 1115 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1173
DB 12484 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12543
QY 1174 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1233
DB 12544 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12603
QY 1234 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1293
DB 12604 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12663
QY 1294 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1353
DB 12664 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12723
QY 1354 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1413
DB 12724 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12782
QY 1414 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1473
DB 12783 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12842
QY 1474 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1533
DB 12843 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12902
QY 1534 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1593
DB 12903 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 12962
QY 1594 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 1653
DB 12963 AATGACCTTCCCAAGATGCTGCGCAATACCTCCAGGAATTCCTTGGCATCTAT 13022
QY 1654 A 1654
DB 13023 A 13023

RESULT 6
US-10-467-252-52
/ Sequence 52, Application US/10467252
/ Publication No. US20040115676A1
/ GENERAL INFORMATION:
/ APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
/ APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
/ APPLICANT: YAO, Monique G.; KALICKI, Deborah A.;
/ APPLICANT: GANDHI, Ameena R.; CHAWLA, Rinder K.;
/ APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
/ APPLICANT: HAFALIA, April J.A.; RAMKUMAR, Jayalaxmi;
/ APPLICANT: JIN, Pei; TANG, Y. Tom;
/ APPLICANT: YUE, Henry; REDDY, Roopa
/ APPLICANT: BURFORD, Neil; LU, Dying Aina M.;
/ APPLICANT: GRAUD, Richard C.; KAHN, Parrah A.;
/ APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
/ APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
/ APPLICANT: WARREN, Bridget A.; YANG, Junning;
/ APPLICANT: LEE, Ernestine A.; HARLAND, Lee


```

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 52
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 90012430CB1
; US-10-467-252-52

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Query Match 73.0%; Score 1228.6; DB 19; Length 1336;

Best Local Similarity 99.6%; Pred. No. 0; Matches 124; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 29 TCTTCAAGCATGATTTTCAACAATTTAAATGGAAGTGTAGACTGATTAAGAGATGC 88
DB 77 TTTTCAAGCATGATTTTCAACAATTTAAATGGAAGTGTAGACTGATTAAGAGATGC 136
QY 89 TCAAGTAAAGGAGTCTCTGATGAGCTTTGATGATGATACCAATCTCTGAAATTGCAT 148
DB 137 TCAGCTAAGGAGAGTCTCTGATGAGCTTTGATGATGATACCAATCTCTGAAATTGCAT 196
QY 149 GCAAAAATGTGACTTCCCAAGTATGCTGAGCAACAACTCCAGAAATTCCTTTCGCA 208
DB 197 GCAAAAATGTGACTTCCCAAGTATGCTGAGCAACAACTCCAGAAATTCCTTTCGCA 256
QY 209 TCCATAGTACACCCCACTTAATCAGCTCTACTGATGATGATGATGATGATGATGAT 268
DB 257 TCCATAGTACACCCCACTTAATCAGCTCTACTGATGATGATGATGATGATGATGAT 316
QY 269 GGGGTGATTTGATTTCTTCTCTCTGATGAAATGAAACCCGGTCACTGACCAACAT 328
DB 317 GGGGTGATTTGATTTCTTCTCTCTGATGAAATGAAACCCGGTCACTGACCAACAT 376
QY 329 GGGGTGATTTGATTTCTTCTCTCTGATGAAATGAAACCCGGTCACTGACCAACAT 388
DB 377 GGGGTGATTTGATTTCTTCTCTCTGATGAAATGAAACCCGGTCACTGACCAACAT 436
QY 389 GACCTACCTCATGACAAAGACTTGAATGTTGGGCTGCCCTTTCGCAAAATTTGATGATG 448
DB 437 GACCTACCTCATGACAAAGACTTGAATGTTGGGCTGCCCTTTCGCAAAATTTGATGATG 496
QY 449 CATGCTGACATCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
DB 497 CATGCTGACATCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
QY 509 ATACCTCATTTCTTCAAGTACAAAGCAAGAGATTTTCAAGAAATTCGATGATGATG 568
DB 557 ATACCTCATTTCTTCAAGTACAAAGCAAGAGATTTTCAAGAAATTCGATGATGATG 616
QY 569 GAGTGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 628

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DB 617 GGCTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 676
QY 629 CCGGTATGAAATTCATGAGGAATPACATGAGAGCATGTTTAAATTTCAAAAGAGCT 688
DB 677 CCGGTATGAAATTCATGAGGAATPACATGAGAGCATGTTTAAATTTCAAAAGAGCT 736
QY 689 TGCTTACACATGATGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 748
DB 737 TGCTTACACATGATGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 796
QY 749 TGATATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 808
DB 797 TGATATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 856
QY 809 CTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
DB 857 CTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 916
QY 869 CATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 928
DB 917 CATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 976
QY 929 GCAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 988
DB 977 GCAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
QY 989 AGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1048
DB 1037 AGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
QY 1049 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1108
DB 1097 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1156
QY 1109 ATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
DB 1157 ATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1216
QY 1168 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1227
DB 1217 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1276
QY 1228 CCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1274
DB 1277 CCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323

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RESULT 7

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US-10-017-161-1193
; Sequence 1193, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIHO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G-PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1318)
; FEATURE:
; NAME/KEY: CDS

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/ LOCATION: (201) .. (1118)
US-10-017-161-1193

Query Match      66.4%; Score 1118.8; DB 15; Length 1318;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 155 ATGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGAAATTCCTCTTGACATCTAT 214
    |||||
DB 185 AGGTGACTTCCCAAGTATGCTGGCCCAATATCTCCAGAAATTCCTCTTGACATCTAT 244

QY 215 AGTGACACCCCACTTAATCAAGCTTCACTTCAATAGTCTTATTGGCGGGCTGGTGGTGT 274
    |||||
DB 245 AGTGACACCCCACTTAATCAAGCTTCACTTCAATAGTCTTATTGGCGGGCTGGTGGTGT 304

QY 275 CATTTCATCTTTCTTCTCTGCTGTAAGAAACACCCGGTCAAGTACCAACCAATGGCGGT 334
    |||||
DB 305 CATTTCATCTTTCTTCTCTGCTGTAAGAAACACCCGGTCAAGTACCAACCAATGGCGGT 364

QY 335 CATTAACTTGGTGGTGGTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTA 394
    |||||
DB 365 CATTAACTTGGTGGTGGTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTA 424

QY 395 CCTCATCAAGAAAGACTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTCCATGCT 454
    |||||
DB 425 CCTCATCAAGAAAGACTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTCCATGCT 484

QY 455 GCACATCCCAATGTACTCTCACTCTCTATCTATGTGTATCTCTGCTCAACCAATACCT 514
    |||||
DB 485 GCACATCCCAATGTACTCTCACTCTCTATCTATGTGTATCTCTGCTCAACCAATACCT 544

QY 515 CATCTTCTTCAAGTGCACAAAGAAAGTATCTACAGAAACCTGATCTGTGGCTGC 574
    |||||
DB 545 CATCTTCTTCAAGTGCACAAAGAAAGTATCTACAGAAACCTGATCTGTGGCTGC 604

QY 575 CAGTGTCTGGGATGTGACGCTGTGTATGTCAATGTGTGTAACCCCTGTGTCTCCGGTA 634
    |||||
DB 605 CAGTGTCTGGGATGTGACGCTGTGTATGTCAATGTGTGTAACCCCTGTGTCTCCGGTA 664

QY 635 TGTAAATCCAGAGAAATACAAATGAGAGCACTGTTTAAATTTACAAAGAGCTTGTGTA 694
    |||||
DB 665 TGTAAATCCAGAGAAATACAAATGAGAGCACTGTTTAAATTTACAAAGAGCTTGTGTA 724

QY 695 CACATATGTAAATATCATCACTATATATAGTCAATTTTGTGATAGCCGTCTGTGAT 754
    |||||
DB 725 CACATATGTAAATATCATCACTATATATAGTCAATTTTGTGATAGCCGTCTGTGAT 784

QY 755 TCTGTGTGTCTTCCAGGTCTTCAATTAATGTGTGATGTGACAGAAAGCTACGCCATCTTT 814
    |||||
DB 785 TCTGTGTGTCTTCCAGGTCTTCAATTAATGTGTGATGTGACAGAAAGCTACGCCATCTTT 844

QY 815 ACTATCCCAACAGAGATTTGGGCTGACGTGAAACCTATTTTATATAGGGTCAATCCT 874
    |||||
DB 845 ACTATCCCAACAGAGATTTGGGCTGACGTGAAACCTATTTTATATAGGGTCAATCCT 904

QY 875 TGTGTGTGTCTTCCCTACAGTTCTTATAGATCTATTACTTGAATTTGTGACGATTC 934
    |||||
DB 905 TGTGTGTGTCTTCCCTACAGTTCTTATAGATCTATTACTTGAATTTGTGACGATTC 964

QY 935 CAATGCTGTAGACAGCAAGTGTGATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 994
    |||||
DB 965 CAATGCTGTAGACAGCAAGTGTGATTTTAAAGAAATCTTCTGAGTGAACAGCAAT 1024

QY 995 TACGTGTATGATTTGTCTCTTCTTGTGTTGGGGAGAGCATTTGTTTAAAGAAAGAT 1054
    |||||
DB 1025 TACGTGTATGATTTGTCTCTTCTTGTGTTGGGGAGAGCATTTGTTTAAAGAAAGAT 1084

QY 1055 AATTGGCTTATGAAATGTGTTTGTGCGCTTGAAGCAACAATACAGTATTCATTTTGC 1114
    |||||
DB 1085 AATTGGCTTATGAAATGTGTTTGTGCGCTTGAAGCAACAATACAGTATTCATTTTGC 1144

QY 1115 TTCCTTTATATTTGGGAAT-AAAAATGGGTATAGGGAGATTAAGATGGTATTTCAATTA 1173
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DB 1145 TTCCTTTATATTTGGGAATTAATAATGGGTATAGGGAGGTAAAGTATTTCAATTA 1204

QY 1174 GATCAAAACCATGCTTGTATGTATACCAAAACAAAGAGACTATTAATGCAAGGCCCTCA 1233
    |||||
DB 1205 GATCAAAACCATGCTTGTATGTATACCAAAACAAAGAGACTATTAATGCAAGGCCCTCA 1264

QY 1234 TTGTAGTCTTATAGGATCCCTCCCATCTCTGATGTATGGCGGTACAAAGACCA 1287
    |||||
DB 1265 TTGTAGTCTTATAGGATCCCTCCCATCTCTGATGTATGGCGGTACAAAGACCA 1318

RESULT 8
US-10-467-252-53
; Sequence 53, Application US/10467252
; Publication No. US20040115676A1
GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HARALIA, April J.A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; YANG, Y.Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dying Anna M.;
; APPLICANT: GRAUB, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; HARLAND, Lee;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 90012586CB1
; US-10-467-252-53

Query Match      65.7%; Score 1106.2; DB 19; Length 1340;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 273 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 332
DB 325 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 384
QY 333 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 392
DB 385 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 444
QY 393 TACCTATCAAGAAAGCTTGGATTTGGGCTGCTGCTTGCAGTAAATTTGAGTGCATG 452
DB 445 TACCTATCAAGAAAGCTTGGATTTGGGCTGCTGCTTGCAGTAAATTTGAGTGCATG 504
QY 453 CTGACATCAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
DB 505 CTGACATCAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
QY 513 CTGATCTTCTTCAAGTCAAGAAAGCTTGGATTTGGGCTGCTGCTGCTGCTGCTGCTGCT 572
DB 565 CTGATCTTCTTCAAGTCAAGAAAGCTTGGATTTGGGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 573 GCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
DB 625 GCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
QY 633 TATGAATCCATGAGAAATCAATGAGAGACCTGTTTAAATTTTCAAGAAAGCTTGGCT 692
DB 685 TATGAATCCATGAGAAATCAATGAGAGACCTGTTTAAATTTTCAAGAAAGCTTGGCT 744
QY 693 TACACATATGTAAGAAATCAATGAGAGACCTGTTTAAATTTTCAAGAAAGCTTGGCT 752
DB 745 TACACATATGTAAGAAATCAATGAGAGACCTGTTTAAATTTTCAAGAAAGCTTGGCT 804
QY 753 ATTCTGTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
DB 805 ATTCTGTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
QY 813 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAGAAACCTATTTTAAAGGGGCTGCT 872
DB 865 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAGAAACCTATTTTAAAGGGGCTGCT 924
QY 873 CTGTTGTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
DB 925 CTGTTGTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
QY 933 TCCAAATGCTGTAAGCAAGAGTTCATTTTAAAGAAATCTTCTGAGTGAACGCA 992
DB 985 TCCAAATGCTGTAAGCAAGAGTTCATTTTAAAGAAATCTTCTGAGTGAACGCA 1044
QY 993 ATTAGCTGTAAGTTCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
DB 1045 ATTAGCTGTAAGTTCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
QY 1053 ATAAATGCTTATGTAAGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
DB 1105 ATAAATGCTTATGTAAGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
QY 1113 GCTTCTTCTTATTTGGGAAT-AAATGCTGTAAGGGAGTAAAGATGTAATTCATTAAC 1171
DB 1165 GCTTCTTCTTATTTGGGAATAAATGCTGTAAGGGAGTAAAGATGTAATTCATTAAC 1224
QY 1172 TTGATCAAAACCAATGCTGTAAGTAAACCAAAAGCTATTAATTTGCAAGAGCCCT 1231
DB 1225 TTGATCAAAACCAATGCTGTAAGTAAACCAAAAGCTATTAATTTGCAAGAGCCCT 1284
QY 1232 CATTTGATGCTTATGAGGATCCCTCCCATCTGAGTATGAGC 1274
DB 1285 CATTTGATGCTTATGAGGATCCCTCCCATCTGAGTATGAGC 1327

RESULT 9
US-10-467-252-54
; Sequence 54, Application US/10467252
; Publication No. US20040115676A1

GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HAPALIA, April J.A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y. Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; Lu, Dying Aina M.;
; APPLICANT: GRAUL, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFPIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junning;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Inocyte ID No: 90012670CB1
; US-10-467-252-54
Query Match 65.7%; Score 1106.2; DB 19; Length 1460;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 153 AAATGACTTCCCAAGTATGCTGCGCAAAATACCTCCAGAAATCTCTTGCATTCCT 212
DB 325 ACAGGTGACTTCCCAAGTATGCTGCGCAAAATACCTCCAGAAATCTCTTGCATTCCT 384
QY 213 AATAGTACACCCCACTTATTCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 272
DB 385 AATAGTACACCCCACTTATTCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 444
QY 273 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 332
DB 445 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 504
QY 453 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 512
DB 505 GTCATTTTCATTTCTTCTCTGAGTAAATGAACCCGGTGCAGTACCAACCATGGCG 564
QY 565 TACCTATCAAGAAAGCTTGGATTTGGGCTGCTGCTTGCAGTAAATTTGAGTGCATG 624
DB 625 TACCTATCAAGAAAGCTTGGATTTGGGCTGCTGCTTGCAGTAAATTTGAGTGCATG 684

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QY 513 CTCATCTTCTTCAAGTCAAGCAAGCAAGTGAATTCATACAGAAACGATGCTGAGCT 572
DB 685 CTCATCTTCTTCAAGTCAAGCAAGCAAGTGAATTCATACAGAAACGATGCTGAGCT 744
QY 573 GCCAGTGTGGCATGTGAGCGCTGTGATTTGATTTGATGATCCCTGATTTGATCCCG 632
DB 745 GCCAGTGTGGCATGTGAGCGCTGTGATTTGATTTGATGATCCCTGATTTGATCCCG 804
QY 633 TATGGAATCCATGAGGAATTCATATGAGAGCATCTGTTTAAATTTTCACAAAGCTTGTCT 692
DB 805 TATGGAATCCATGAGGAATTCATATGAGAGCATCTGTTTAAATTTTCACAAAGCTTGTCT 864
QY 693 TACACATATGTAATTCATCACTATGATGATGATGATGATGATGATGATGATGATGATG 752
DB 865 TACACATATGTAATTCATCACTATGATGATGATGATGATGATGATGATGATGATGATG 924
QY 753 ATTCTGTGTGCTTCCAGGTCTTTCATCATTATGATGATGATGATGATGATGATGATGATG 812
DB 925 ATTCTGTGTGCTTCCAGGTCTTTCATCATTATGATGATGATGATGATGATGATGATGATGATG 984
QY 813 TTAATATCCCAACGAGATTTGAGGCTGAGCTGAGTGAATAAATCTATTTTATAGGGGTCATC 872
DB 985 TTAATATCCCAACGAGATTTGAGGCTGAGCTGAGTGAATAAATCTATTTTATAGGGGTCATC 1044
QY 873 CTGTGTTGTTTCTTCCCTACAGTCTTTCATGATGATGATGATGATGATGATGATGATGATG 932
DB 1045 CTGTGTTGTTTCTTCCCTACAGTCTTTCATGATGATGATGATGATGATGATGATGATGATG 1104
QY 933 TCCAAATGCTGTGAGCAAGGTTGATTTATTAACGAAATCTTCTTGAAGTGTACAGCA 992
DB 1105 TCCAAATGCTGTGAGCAAGGTTGATTTATTAACGAAATCTTCTTGAAGTGTACAGCA 1164
QY 993 ATTAAGTGTGATATTTGCTTCTTGTGTTGGGGAAGCAATGGTTTAAAGCAAAAG 1052
DB 1165 ATTAAGTGTGATATTTGCTTCTTGTGTTGGGGAAGCAATGGTTTAAAGCAAAAG 1224
QY 1053 ATTAAGTGTGATATTTGCTTCTTGTGTTGGGGAAGCAATGGTTTAAAGCAAAAG 1112
DB 1225 ATTAAGTGTGATATTTGCTTCTTGTGTTGGGGAAGCAATGGTTTAAAGCAAAAG 1284
QY 1113 GCTTCCTTATATTTGGGAAT-AAATGGGTATAGGGGAGTAAAGTGTATTTCAATTC 1171
DB 1285 GCTTCCTTATATTTGGGAAT-AAATGGGTATAGGGGAGTAAAGTGTATTTCAATTC 1344
QY 1172 TTGATCAAAACCATGCTTGAATGATCAACCAAAACCAAAAGCATTAATAAGCAAGACCTCT 1231
DB 1345 TTGATCAAAACCATGCTTGAATGATCAACCAAAACCAAAAGCATTAATAAGCAAGACCTCT 1404
QY 1232 CATTTAGTCTTATGAGGATCCCTCCCATCTCTGATGATGAGC 1274
DB 1405 CATTTAGTCTTATGAGGATCCCTCCCATCTCTGATGATGAGC 1447

RESULT 10
US-10-398-036-22
; Sequence 22, Application US/10398036
; Publication No. US20040137564A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL, Richard C.; CHAWLA, Nandinder K.;
; APPLICANT: RAMKUMAR, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyrung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
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; CURRENT APPLICATION NUMBER: US/10/398,036
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6157025CB1
; US-10-398-036-22

Query Match 61.2%; Score 1030; DB 19; Length 1499;
Best Local Similarity 98.6%; Pred. No. 1.9e-292;
Matches 1091; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

QY 157 GTGACTTCCCAAGTATGCTGTGCAACAATATCTCGAGAAATCTCTTGATCTTATG 216
DB 367 GTGACTTCCCAAGTATGCTGTGCAACAATATCTCGAGAAATCTCTTGATCTTATG 426
QY 217 TGACACCCCACTTAATACAGCTCTTATGATGATGATGATGATGATGATGATGATGATG 276
DB 427 TGACACCCCACTTAATACAGCTCTTATGATGATGATGATGATGATGATGATGATGATG 486
QY 277 TTTCAATCTTTTCTCTCTGTAATAATGAACCCGCTGATGACCAACATGCGGTCA 336
DB 487 TTTCAATCTTTTCTCTCTGTAATAATGAACCCGCTGATGACCAACATGCGGTCA 546
QY 337 TTAATCTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTACC 396
DB 547 TTAATCTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTACC 606
QY 397 TCATCAAGGAAGCTTGATGATTTGGGCTGCTTCTGCAAAATTTGATGATGATGATG 456
DB 607 TCATCAAGGAAGCTTGATGATTTGGGCTGCTTCTGCAAAATTTGATGATGATGATG 666
QY 457 ACATCCACATGATCTCAAGCTTCTATTTCTATGATGATGATGATGATGATGATGATG 516
DB 667 ACATCCACATGATCTCAAGCTTCTATTTCTATGATGATGATGATGATGATGATGATG 726
QY 517 TCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCA 576
DB 727 TCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCA 786
QY 577 GTGCTGGCATGTGAGCGCTGTGATTTGATGATGATGATGATGATGATGATGATGATG 636
DB 787 GTGCTGGCATGTGAGCGCTGTGATTTGATGATGATGATGATGATGATGATGATGATG 846
QY 637 GAATCATGAGGAATTAATGAGAGCACTGTTTAAATTTTCACAAAGAGCTTGCTTACA 696
DB 847 GAATCATGAGGAATTAATGAGAGCACTGTTTAAATTTTCACAAAGAGCTTGCTTACA 906
QY 697 CATATGTGAATAATCAATCAATATATGATGATTTTGTCTATGACCGTGTGCTGATTC 756
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/ PRIOR FILING DATE: 2001-03-01
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 939
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(939)
US-10-085-233B-3

Query Match      55.8%; Score 939; DB 14; Length 939;
Best Local Similarity 100.0%; Pred. No. 1e-265;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      147  ATGCAAAATGTACTTCCCAAGTAGCCGCGCACAAATCCTCCAGAAATTCCTCTTGC 206
      1  ATGCAAAATGTACTTCCCAAGTAGCCGCGCACAAATCCTCCAGAAATTCCTCTTGC 60
QY      207  GATCTATAGTGACACCCCACTTAATCAGCCTCTACTCTTCAAGTGTATTGGCGGCGT 266
      61  GATCTATAGTGACACCCCACTTAATCAGCCTCTACTCTTCAAGTGTATTGGCGGCGT 120
QY      267  GTGGGTGTCAATTCATTTCTTCTCTGTGTGAAAAATGAACCCCGTCAGTACACC 326
      121  GTGGGTGTCAATTCATTTCTTCTCTGTGTGAAAAATGAACCCCGTCAGTACACC 180
QY      327  ATGGCGGTCAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 386
      181  ATGGCGGTCAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY      387  TTGACCTACTCATCAAGAAAGACTTGGATGTGGGCTGCGCTTGCAGAAATTTGTGAGT 446
      241  TTGACCTACTCATCAAGAAAGACTTGGATGTGGGCTGCGCTTGCAGAAATTTGTGAGT 300
QY      447  GCCATGCTGACATTCACATGATGATCTCAAGTCTTCTATGTGTGTGTGTGTGTGTGT 506
      301  GCCATGCTGACATTCACATGATGATCTCAAGTCTTCTATGTGTGTGTGTGTGTGTGT 360
QY      507  AGATTAATCTATCTTTTCAAGTGTGAAAGAAAGTGTGAAATTTCAAGAAATTCGATGCT 566
      361  AGATTAATCTATCTTTTCAAGTGTGAAAGAAAGTGTGAAATTTCAAGAAATTCGATGCT 420
QY      567  GTGGGTGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626
      421  GTGGGTGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY      627  TCCCGGTATGAAATTCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAGAAAG 686
      481  TCCCGGTATGAAATTCATGAGAAATCAATGAGAGCACTGTTTAAATTTCAAGAAAG 540
QY      687  CTGGCTTAACATATGTGAAATTCATGATGATGATGATGATGATGATGATGATGATGAT 746
      541  CTGGCTTAACATATGTGAAATTCATGATGATGATGATGATGATGATGATGATGATGAT 600
QY      747  GGTGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 806
      601  GGTGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY      807  CACTCTTTAATCAACCAAGAGTCTGGGCTCAGCTGAAAAAATTTTATATATATATAT 866
      661  CACTCTTTAATCAACCAAGAGTCTGGGCTCAGCTGAAAAAATTTTATATATATATAT 720
QY      867  GTCAATCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 926
      721  GTCAATCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY      927  AGCATTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 986
      781  AGCATTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY      987  ACAGCAATTAGCTGTATGATTTGCTTCTTTGTCTTTGGGGGAAAGCAATGGTTAAG 1046
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DB      841  ACAGCAATTAGCTGTATGATTTGCTTGTCTTTGGGGGAAAGCAATGGTTAAG 900
QY      1047  CAAAAGATAATGGCTTATGAAATTTGTTTGTGCGGT 1085
      901  CAAAAGATAATGGCTTATGAAATTTGTTTGTGCGGT 939

RESULT 13
US-09-995-225-3
/ Sequence 3, Application US/09995225
/ Publication No. US20020193584A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Chen, Zhi Liang
/ APPLICANT: Dang, Huang T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Pride, Cameron
/ TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
/ FILE REFERENCE: AREN-0308
/ CURRENT APPLICATION NUMBER: US/09/995,225
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: PCT/US99/23938
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/253,404
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/255,366
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: 60/270,286
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/282,365
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/270,266
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/282,032
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,358
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,356
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/290,917
/ PRIOR FILING DATE: 2001-05-14
/ PRIOR APPLICATION NUMBER: 60/309,208
/ PRIOR FILING DATE: 2001-07-31
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 918
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-995-225-3

Query Match      54.4%; Score 916.4; DB 9; Length 918;
Best Local Similarity 99.9%; Pred. No. 4.7e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      171  ATGCTGGCCACATATCTCCAGAAATTCCTTTGGATCTATATGTGACACCCACTTA 230
      1  ATGCTGGCCACATATCTCCAGAAATTCCTTTGGATCTATATGTGACACCCACTTA 60
QY      231  ATCAGCTCTACTTATATGTGCTTATTTGGCGGGCTGGTGGGTGATTTCCATTCCTTTC 290
      61  ATCAGCTCTACTTATATGTGCTTATTTGGCGGGCTGGTGGGTGATTTCCATTCCTTTC 120
QY      291  CTCCTGTGAAATGAACAACCCGTCAGTGAACCAATGCGCGTCAATTAATCTGTGTGTG 350
      121  CTCCTGTGAAATGAACAACCCGTCAGTGAACCAATGCGCGTCAATTAATCTGTGTGTG 180
QY      351  GTCCAGCGTTTTTCTGTGTGACAGTGCATTTGCTTGAATCTTCACTCAAGAAAGACT 410
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Db	601	GGCTTCATCATATTATGTGATGTGACGAAGCTACGCCACTCTTTACTATCCACCGAGG	600
Qy	771	GGCTTCATCATATTATGTGATGTGACGAAGCTACGCCACTCTTTACTATCCACCGAGG	830
Db	541	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGTGCTGATTCGTGTGCTTCAG	770
Qy	711	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGTGCTGATTCGTGTGCTTCAG	770
Db	481	TACAAATGAGAGCACTGTTTTAAATTTCACAAAAGACTTGCTTACATATGGAATTC	540
Qy	651	TACAAATGAGAGCACTGTTTTAAATTTCACAAAAGACTTGCTTACATATGGAATTC	710
Db	421	ACGCTGGGATGTCATTTGTGTGACCCCGGTGTGTCCTCCGGATAGGAATTCATGAGAA	480
Qy	591	ACGCTGGGATGTCATTTGTGTGACCCCGGTGTGTCCTCCGGATAGGAATTCATGAGAA	650
Db	361	AAAAGCAAAAGTGAATTTCTACAGAAAACTCATGCTGTGTGCTGCCAGTGTGCATGTG	420
Qy	531	AAAAGCAAAAGTGAATTTCTACAGAAAACTCATGCTGTGTGCTGCCAGTGTGCATGTG	590
Db	301	CTCAGGTTCTATTTCTATGTGTGTAATCTGTGACCAAGATACCTATCTTTCAAGTGC	360
Qy	471	CTCAGGTTCTATTTCTATGTGTGTAATCTGTGACCAAGATACCTATCTTTCAAGTGC	530
Db	241	TGGATGTTGGGCTGCCCTCTTCGCAAAATTTGTAGAGCCATGCTGCACATCCACATGTAC	300
Qy	411	TGGATGTTGGGCTGCCCTCTTCGCAAAATTTGTAGAGCCATGCTGCACATCCACATGTAC	470
Db	181	GTCCACAGAGGTTTTCTGTGTGACAGTGCATTTGCTTGAACCTCATCAAGAAACT	240
Qy	351	GTCCACAGAGGTTTTCTGTGTGACAGTGCATTTGCTTGAACCTCATCAAGAAACT	410
Db	121	CTCCTGTGAAATATGAACACCCGGTCAAGACCAACCATGGCGGTCAATTAATTGGTGTG	350
Qy	291	CTCCTGTGAAATATGAACACCCGGTCAAGACCAACCATGGCGGTCAATTAATTGGTGTG	290
Db	61	ATCAGCCTCTACTCTTCAATATGTGCTATGTGCGGGCTGTGTGTGCTATTTCCATTTTTC	120
Qy	231	ATCAGCCTCTACTCTTCAATATGTGCTATGTGCGGGCTGTGTGTGCTATTTCCATTTTTC	230
Db	1	ATGCTCGGCACAAATACCTCCAGGAATTCCTCTTGGATCTATATGTGACACCCCACTTA	60
Qy	171	ATGCTCGGCACAAATACCTCCAGGAATTCCTCTTGGATCTATATGTGACACCCCACTTA	230
Db	1	ATGCTCGGCACAAATACCTCCAGGAATTCCTCTTGGATCTATATGTGACACCCCACTTA	60
Qy	231	ATCAGCCTCTACTCTTCAATATGTGCTATGTGCGGGCTGTGTGTGCTATTTCCATTTTTC	230
Db	61	ATCAGCCTCTACTCTTCAATATGTGCTATGTGCGGGCTGTGTGTGCTATTTCCATTTTTC	120
Qy	291	CTCCTGTGAAATATGAACACCCGGTCAAGACCAACCATGGCGGTCAATTAATTGGTGTG	350
Db	121	CTCCTGTGAAATATGAACACCCGGTCAAGACCAACCATGGCGGTCAATTAATTGGTGTG	180
Qy	351	GTCCACAGAGGTTTTCTGTGTGACAGTGCATTTGCTTGAACCTCATCAAGAAACT	410
Db	181	GTCCACAGAGGTTTTCTGTGTGACAGTGCATTTGCTTGAACCTCATCAAGAAACT	240
Qy	411	TGGATGTTGGGCTGCCCTCTTCGCAAAATTTGTAGAGCCATGCTGCACATCCACATGTAC	470
Db	241	TGGATGTTGGGCTGCCCTCTTCGCAAAATTTGTAGAGCCATGCTGCACATCCACATGTAC	300
Qy	471	CTCAGGTTCTATTTCTATGTGTGTAATCTGTGACCAAGATACCTATCTTTCAAGTGC	530
Db	301	CTCAGGTTCTATTTCTATGTGTGTAATCTGTGACCAAGATACCTATCTTTCAAGTGC	360
Qy	531	AAAAGCAAAAGTGAATTTCTACAGAAAACTCATGCTGTGTGCTGCCAGTGTGCATGTG	590
Db	361	AAAAGCAAAAGTGAATTTCTACAGAAAACTCATGCTGTGTGCTGCCAGTGTGCATGTG	420
Qy	591	ACGCTGGGATGTCATTTGTGTGACCCCGGTGTGTCCTCCGGATAGGAATTCATGAGAA	650
Db	421	ACGCTGGGATGTCATTTGTGTGACCCCGGTGTGTCCTCCGGATAGGAATTCATGAGAA	480
Qy	651	TACAAATGAGAGCACTGTTTTAAATTTCACAAAAGACTTGCTTACATATGGAATTC	710
Db	481	TACAAATGAGAGCACTGTTTTAAATTTCACAAAAGACTTGCTTACATATGGAATTC	540
Qy	711	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGTGCTGATTCGTGTGCTTCAG	770
Db	541	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGTGCTGATTCGTGTGCTTCAG	600
Qy	771	GGCTTCATCATATTATGTGATGTGACGAAGCTACGCCACTCTTTACTATCCACCGAGG	830
Db	601	GGCTTCATCATATTATGTGATGTGACGAAGCTACGCCACTCTTTACTATCCACCGAGG	600


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QY      831 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC 890
DB      661 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC 720
QY      891 TACCAATTTCTTATAGATCTTATTAAGTGTGTAAGCATTCGCAATGCTGTAGCAGC 950
DB      721 TACCAATTTCTTATAGATCTTATTAAGTGTGTAAGCATTCGCAATGCTGTAGCAGC 780
QY      951 AAGGTGCAATTTATTAACGAAATCTTGTGATGTAAAGCATTAAGTGTGATGATTTG 1010
DB      781 AAGGTGCAATTTATTAACGAAATCTTGTGATGTAAAGCATTAAGTGTGATGATTTG 840
QY      1011 CTCTCTTTGTCTTTGGGGAGAGCCATGCTTTAAGCAAAAGATTAAGCTTATGGAAT 1070
DB      841 CTCTCTTTGTCTTTGGGGAGAGCCATGCTTTAAGCAAAAGATTAAGCTTATGGAAT 900
QY      1071 TGTGTTTGTGCGCTTAG 1088
DB      901 TGTGTTTGTGCGCTTAG 918

RESULT 15
US-10-055-106C-1
; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Harland, Lee
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: P010970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-055-106C-1

Query Match      54.4%; Score 916.4; DB 14; Length 918;
Best Local Similarity 99.9%; Pred. No. 4,7e-259;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      171 ATGCTGGCCACAATACTTCAGAAATTCCTTTCGATCTTAATAGTGAACCCCACTTA 230
DB      1  ATGCTGGCCACAATACTTCAGAAATTCCTTTCGATCTTAATAGTGAACCCCACTTA 60
QY      231 ATGAGCTCTACTTCAATAGCTTATTTGGGGGCTGTGGGTGTCATTTCCATTTCTTTTC 290
DB      61  ATGAGCTCTACTTCAATAGCTTATTTGGGGGCTGTGGGTGTCATTTCCATTTCTTTTC 120
QY      291 CTCTGGTGAATAATGAACACCCGCTAGTGAACCAACCATGGCGGTCAATTAACCTTGATG 350
DB      121 CTCTGGTGAATAATGAACACCCGCTAGTGAACCAACCATGGCGGTCAATTAACCTTGATG 180
QY      351 GTCACAGCGTTTCTGTGTCAGATGTCATTTGCTTGAACCTTACTCAATCAAGAACT 410
DB      181 GTCACAGCGTTTCTGTGTCAGATGTCATTTGCTTGAACCTTACTCAATCAAGAACT 240
QY      411 TGGATTTTGGGCTGCTTTCGCAAAATTTGTAAGTGCATGTCACATCCACATGTAC 470
DB      241 TGGATTTTGGGCTGCTTTCGCAAAATTTGTAAGTGCATGTCACATCCACATGTAC 300
QY      471 CTCACGTTCTTATTTATGATGATCTGTGTCACAGATTAACCTCAATCTTCTCAAGTGC 530
DB      301 CTCACGTTCTTATTTATGATGATCTGTGTCACAGATTAACCTCAATCTTCTCAAGTGC 360
QY      531 AAAGCAAAAGTGAATTTTACAGAAAAATGCATGCTGTGGCTGCCAGTGGCATGTGG 590
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DB      361 AAAGCAAAAGTGAATTTTACAGAAAAATGCATGCTGTGGCTGCCAGTGGCATGTGG 420
QY      591 AAGCTGAGATTTGATTTGTGTACCCCGTGTGCTCCCGGTATGGAATCATAGAGAA 650
DB      421 AAGCTGAGATTTGATTTGTGTACCCCGTGTGCTCCCGGTATGGAATCATAGAGAA 480
QY      651 TACAATGAGAGACACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGTGAAATC 710
DB      481 TACAATGAGAGACACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGTGAAATC 540
QY      711 ATCAATATATATATGTCATTTTGTGATAGCCGTTGCTGTGATTTGTGCTTCCAG 770
DB      541 ATCAATATATATATGTCATTTTGTGATAGCCGTTGCTGTGATTTGTGCTTCCAG 600
QY      771 GTCCTCATATATGTTGATGTTGAGAGAGTACGCACTCTTATCTATCCACAGAG 830
DB      601 GTCCTCATATATATGTTGATGTTGAGAGTACGCACTCTTATCTATCCACAGAG 660
QY      831 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC 890
DB      661 TTCTGGGCTCAGCTGAAAAAAGCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC 720
QY      891 TACCAATTTCTTATAGATCTTATTAAGTGTGTAAGCATTCGCAATGCTGTAGCAGC 950
DB      721 TACCAATTTCTTATAGATCTTATTAAGTGTGTAAGCATTCGCAATGCTGTAGCAGC 780
QY      951 AAGGTGCAATTTATTAACGAAATCTTGTGATGTAAAGCATTAAGTGTGATGATTTG 1010
DB      781 AAGGTGCAATTTATTAACGAAATCTTGTGATGTAAAGCATTAAGTGTGATGATTTG 840
QY      1011 CTCTCTTTGTCTTTGGGGAGAGCCATGCTTTAAGCAAAAGATTAAGCTTATGGAAT 1070
DB      841 CTCTCTTTGTCTTTGGGGAGAGCCATGCTTTAAGCAAAAGATTAAGCTTATGGAAT 900
QY      1071 TGTGTTTGTGCGCTTAG 1088
DB      901 TGTGTTTGTGCGCTTAG 918
```

Search completed: September 10, 2005, 03:39:13
Job time : 1218.69 secs

PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT disorders.

XX Claim 15; Page 101; 105pp; English.

CC The invention relates to an isolated polypeptide, which is a G-protein
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
CC receptor type proteins (GPCRs), designated the 93870 receptor. The
CC polypeptides, nucleic acid molecules and antibodies of the invention are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC monitoring clinical trials or pharmacogenetics), or in methods of
CC treatment (e.g. therapeutic and prophylactic). They are useful in
CC creating and diagnosing conditions related to aberrant activity or
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC disorders, or bone marrow mononuclear disorders, as well as cellular
CC proliferative and/or differentiative disorders, hormonal disorders,
CC neurological disorders, cardiovascular disorders, viral diseases, liver
CC disorders, and pain and metabolic disorders. Conditions that can be
CC treated include cancer, diabetes mellitus, hypothyroidism,
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC Huntington's disease, heart failure, angina pectoris, myocardial
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC transgenic animals are useful for studying the function and/or activity
CC of a 93870 protein and for identifying and/or evaluating modulators of
CC 93870 activities. The polynucleotides of the invention can be used in
CC gene therapy. This sequence represents the human G-protein coupled
CC receptor type protein of the invention

XX Sequence 313 AA;

Query Match 100.0%; Score 1637; DB 5; Length 313;

Best Local Similarity 100.0%; Pred. No. 9.5e-175; Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMPGHNTRSSCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60
DB 1 MOKCDPSPMPGHNTRSSCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60
QY MAVINLVVHVSFVLTVPFRLTYLIKTTWFGSLPCKPVSAMLHMVLTFLFYVILVT 120
DB 61 MAVINLVVHVSFVLTVPFRLTYLIKTTWFGSLPCKPVSAMLHMVLTFLFYVILVT 120
QY 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180
DB 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180
QY 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180
DB 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180
QY 181 LATTYKILINMIVIVIAVAVALVLPQVFIIMAMQKRLSHLSHQEFMAQIKNLPFTIG 240
DB 181 LATTYKILINMIVIVIAVAVALVLPQVFIIMAMQKRLSHLSHQEFMAQIKNLPFTIG 240
QY 241 VILVCFLPYQFPRITLVVWTHSNACSSKVAFAFNEIFLSTAIACVDLLFPVGGSHMFK 300
DB 241 VILVCFLPYQFPRITLVVWTHSNACSSKVAFAFNEIFLSTAIACVDLLFPVGGSHMFK 300
QY 301 OKIIGLMNCVLCR 313
DB 301 OKIIGLMNCVLCR 313

RESULT 2
AAB71325
ID AAB71325 standard; protein; 313 AA.

XX AAB71325;
XX
XX 19-NOV-2002 (first entry)
XX

DE Human GCREC-4 INCYTE ID 90012430CD1 SEQ ID 4.

XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection; receptor;
XX gene therapy.

OS Homo sapiens.

PN WO200263004-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002MO-US003635.

PR 07-FEB-2001; 2001US-0267322P.

PR 23-FEB-2001; 2001US-0271215P.

PR 08-MAR-2001; 2001US-0274551P.

PR 23-MAR-2001; 2001US-0278507P.

PR 30-MAR-2001; 2001US-0280597P.

PR 02-APR-2001; 2001US-0281107P.

PR 06-APR-2001; 2001US-0282121P.

XX (INCY-) INCYTE GENOMICS INC.

PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;

PI Kallik DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AUA;

PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;

PI Grail RC, Khan FA, Walsh RT, Leon CH, Richardson TW, Griffin JA;

PI Warren BA, Yang J, Lee EA, Harland L;

XX WPI; 2002-627557/67.

DR N-PSDB; AAF8583.

XX New human G-protein coupled receptors (GCREC), useful for diagnosing or

PT treating a disease or condition associated with decreased expression or

PT over expression of functional GCRECs e.g. cancer, Alzheimer's and

PT Parkinson's.

XX Claim 65; Page 164-165; 239pp; English.

XX This invention describes novel polypeptides which have anti-HIV,

CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,

CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,

CC antibacterial, fungicide and protozoacide activity. The products of the

CC invention are useful for treating a disease or condition associated with

CC decreased expression or over expression of functional G-protein coupled

CC receptors (GCREC), while antibodies generated against the polypeptide of

CC the invention are useful for diagnosing a condition or disease associated

CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,

CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,

CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.

CC The compounds described in the invention can be used for gene therapy.

CC AAB71322-AAB71369 represent the GCREC proteins encoded by AAF8580-

CC AAF86827 described in the disclosure of the invention

XX Sequence 313 AA;

Query Match 99.8%; Score 1634; DB 5; Length 313;

Best Local Similarity 99.7%; Pred. No. 2.1e-174; Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMPGHNTRSSCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60
DB 1 MOKCDPSPMPGHNTRSSCDPIVTPHLISLYFIYVILIGLVGISILFLVKNMTRSVTT 60
QY 61 MAVINLVVHVSFVLTVPFRLTYLIKTTWFGSLPCKPVSAMLHMVLTFLFYVILVT 120
DB 61 MAVINLVVHVSFVLTVPFRLTYLIKTTWFGSLPCKPVSAMLHMVLTFLFYVILVT 120
QY 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180
DB 121 RYLIFPKCKDKVEFYRKLHVAASAGMNTLVIVVPLVVSRYGHEEYNEHCFFKHKE 180

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Db      121 RYLFPEKCKDKEFRYRLAHVAASAGMWTIVTVLVPLVVSRYGHEHNEHCFKFKHKE 180
Qy      181 LAYTYVYKINMYIFVIAVAVILLVQVFIIMVMOKLRHSLSHOEFMAOLKNLPFG 240
Db      181 LAYTYVYKINMYIFVIAVAVILLVQVFIIMVMOKLRHSLSHOEFMAOLKNLPFG 240
Qy      241 VILVCFPIYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTVATISCYDLLFVFGSHMPK 300
Db      241 VILVCFPIYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTVATISCYDLLFVFGSHMPK 300
Qy      301 OKIIGLMNCVLCR 313
Db      301 OKIIGLMNCVLCR 313

RESULT 3
AAG80969
ID      AAG80969 standard; protein, 312 AA.
XX
AC      AAG80969;
XX
DT      28-AUG-2001 (first entry)
XX
DE      Human nGRCR16 #2.
XX
KW      G, protein-coupled receptor; nGRCR; seven transmembrane receptor;
KW      signal transduction; schizophrenia; thyroid disorder; renal failure;
KW      rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW      cardiovascular disease; proliferative disorder; hormonal disorder;
KW      neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW      attention deficit-hyperactivity disorder; attention deficit disorder;
KW      Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW      rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW      neuroprotective.
XX
OS      Homo sapiens.
XX
PN      MO200136473-A2.
XX
PD      25-MAY-2001.
XX
PF      16-NOV-2000; 2000MO-US031581.
XX
PR      16-NOV-1999; 99US-0165838P.
PR      17-NOV-1999; 99US-0166071P.
PR      19-NOV-1999; 99US-0166678P.
PR      28-DEC-1999; 99US-0173396P.
PR      22-FEB-2000; 2000US-0184129P.
PR      28-FEB-2000; 2000US-0185421P.
PR      28-FEB-2000; 2000US-0185549P.
PR      02-MAR-2000; 2000US-0186530P.
PR      03-MAR-2000; 2000US-0186811P.
PR      09-MAR-2000; 2000US-0188114P.
PR      17-MAR-2000; 2000US-0190310P.
PR      21-MAR-2000; 2000US-0190800P.
PR      20-APR-2000; 2000US-0198588P.
PR      02-MAY-2000; 2000US-0201190P.
PR      08-MAY-2000; 2000US-0203111P.
PR      25-MAY-2000; 2000US-0207094P.
XX
PA      (PHMA ) PHARMACIA & UPJOHN CO.
XX
PI      Vogel I, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J,
XX      Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX      WPI; 2001-369826/41.
XX      N-PSDB; AAHS1009.
XX      New G protein-coupled receptor (nGRCR-x) and its encoding polynucleotide
XX      useful for diagnosing and treating e.g. schizophrenia.
XX      Claim 37; Page 90; 261pp; English.

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XX      The present invention relates to novel G protein-coupled receptors
CC      (nGRCR); where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC      31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC      one such G protein-coupled receptor. GPCRs are also known as seven
CC      transmembrane receptors and function in signal transduction. The nGRCR
CC      coding sequences are useful for screening a human to diagnose a disorder
CC      affecting the brain or a genetic predisposition, specifically
CC      schizophrenia. nGRCR are useful for identifying compounds useful for
CC      treating schizophrenia. Detection of nGRCR in a sample is useful as a
CC      diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC      failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC      metabolic and cardiovascular diseases, proliferative disorders and
CC      hormonal disorders. Modulators of nGRCR activity have the utility for
CC      treating neurological disorders, including schizophrenia, ADHD/ADD
CC      (attention deficit-hyperactivity disorder/attention deficit disorder),
CC      and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC      migraine and senile dementia. Additional disorders include inflammatory
CC      conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC      disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC      diseases e.g. inflammatory bowel disease
XX
SQ      Sequence 312 AA;
XX
Query Match      98.4%; Score 1610; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 1e-171;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      5 DPFSGMGHNTSRSSCDPIVTPHLISLYFVILIGLVGVISILFLVKNMTRSVTTMAVI 64
Db      4 DPFSGMGHNTSRSSCDPIVTPHLISLYFVILIGLVGVISILFLVKNMTRSVTTMAVI 63
Qy      65 NLVVHVSVELLYVPFRILYIKKTMFGLPCKFVSAMLIHMYLTFLLPVVILVTRYLI 124
Db      64 NLVVHVSVELLYVPFRILYIKKTMFGLPCKFVSAMLIHMYLTFLLPVVILVTRYLI 123
Qy      125 FPKCKDKVEFRYRLAHVAASAGMWTIVTVLVPLVVSRYGHEHNEHCFKFKELAYT 184
Db      124 FPKCKDKVEFRYRLAHVAASAGMWTIVTVLVPLVVSRYGHEHNEHCFKFKELAYT 183
Qy      185 YKINMYIFVIAVAVILLVQVFIIMVMOKLRHSLSHOEFMAOLKNLPFGIYIV 244
Db      184 YKINMYIFVIAVAVILLVQVFIIMVMOKLRHSLSHOEFMAOLKNLPFGIYIV 243
Qy      245 CFLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTVATISCYDLLFVFGSHMPKQKI 304
Db      244 CFLPYQPFRIYYLNVVTHSNAGSKVAFYNEIFLSTVATISCYDLLFVFGSHMPKQKI 303
Qy      305 GLMNCVLCR 313
Db      304 GLMNCVLCR 312

RESULT 4
ABG93787
ID      ABG93787 standard; protein, 312 AA.
XX
AC      ABG93787;
XX
DT      26-NOV-2002 (first entry)
XX
DE      Human G protein-coupled receptor protein, nGRCR-16.
XX
KW      Human; receptor; G protein-coupled receptor; GPCR; nGRCR; beGRCR;
KW      nG protein coupled receptor; communication; serpentine structure;
KW      seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW      genetic predisposition; brain; immune response; gene therapy;
KW      anxiety disorder; depression; bipolar disorder; schizophrenia;
KW      Huntington's disease; dyskinesia; manic depression; stroke;
KW      Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW      tranquiliser.
XX
OS      Homo sapiens.

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XX WO200264789-A1.
 XX
 XX 22-AUG-2002.
 XX
 XX 14-FEB-2001; 2001WO-US004641.
 XX
 XX 14-FEB-2001; 2001WO-US004641.
 XX
 XX (PHMA) PHARMACIA & UPJOHN CO.
 XX
 XX Lind P, Parodi LA, Vogeli G, Wood LS;
 XX
 XX WPI; 2002-674879/72.
 XX
 XX N-PSDB; ABS70242.
 XX
 XX
 XX New nucleic acids and polypeptides of the ng protein-coupled receptor,
 PT useful for treating or diagnosing a mental disorder or a disorder
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
 PT Parkinson's disease.
 XX
 XX
 XX Example 1; Page 85; 244pp; English.

XX The invention discloses an isolated human polypeptide, and encoding
 CC nucleic acid, for a G-protein-coupled receptor (GPCR), particularly the
 CC ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the
 CC communication between cells and their environment and are characterised
 CC by a serpentine structure that passes through the cell membrane seven
 CC times, hence the reason such receptors are sometimes called seven
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
 CC useful for identifying an ngPCR allelic variant that correlates with a
 CC mental disorder, for isolating an antibody that binds to an epitope of
 CC the polypeptide, for identifying a compound that binds the polypeptide or
 CC polynucleotide and/or modulates its biological activity, for screening a
 CC human subject to diagnose a disorder, or a genetic predisposition to a
 CC disorder, affecting the brain or a genetic disposition to the disorder,
 CC for identifying compounds useful for the treatment of a mental disorder,
 CC and for identifying a compound useful as a modulator of binding between
 CC ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also
 CC useful for inducing an immune response in a mammal. The nucleic acid or
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
 CC be used for treating diabetes, inflammation or wounds. The sequences
 CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the ngPCR (also
 CC referred to as beGPCR) proteins
 XX
 XX Sequence 312 AA;

Query Match 98.4%; Score 1610; DB 5; Length 312;
 Best Local Similarity 99.7%; Pred. No. 1e-171; 0; Indels 0; Gaps 0;
 Matches 308; Conservative 1; Mismatches 0;
 QY 5 DEPSMFGHNTSRNSCDPIVTPHLISLYFIVLIGLVGVISILFLVKNMTRSVTTMAVI 64
 PS |||||
 DB 4 DEPSMFGHNTSRNSCDPIVTPHLISLYFIVLIGLVGVISILFLVKNMTRSVTTMAVI 63
 QY 65 NLVNVHVSFLVLTVPFRLTYLIKTTWFGLPCKCFVSAMHIMHYLTFLPYVILVTRYL 124
 PS |||||
 DB 64 NLVNVHVSFLVLTVPFRLTYLIKTTWFGLPCKCFVSAMHIMHYLTFLPYVILVTRYL 123
 QY 125 FPKCKDKEFEYRLKLVVAVASAGMWTIVIVVPLVVSRYGHEHYNEECFPHKELATV 184
 PS |||||
 DB 124 FPKCKDKEFEYRLKLVVAVASAGMWTIVIVVPLVVSRYGHEHYNEECFPHKELATV 183
 QY 185 YKIIINMIVIFVIAVAVILLVFOVEIIMLVOKLRHSLLSHQEFMAQDKNLEFFIGVILV 244
 PS |||||
 DB 184 YKIIINMIVIFVIAVAVILLVFOVEIIMLVOKLRHSLLSHQEFMAQDKNLEFFIGVILV 243
 QY 245 CFLPYQFPRFIYIANTVTHSNACSSKAPFNEIFLSTATAISCDLLFLVGGSHWFQKXII 304
 PS |||||
 DB 244 CFLPYQFPRFIYIANTVTHSNACSSKAPFNEIFLSTATAISCDLLFLVGGSHWFQKXII 303

QY 305 GLMNCVLCR 313
 |||||
 DB 304 GLMNCVLCR 312

RESULT 5
 AAB71327
 ID AAB71327 standard; protein; 367 AA.

AC AAB71327;

DT 19-NOV-2002 (first entry)

DE Human GCREC-6 INCYTE ID 90012670CD1 SEQ ID 6.

XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
 XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
 XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
 XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
 XX Parkinson's disease; Crohn's disease; constipation; infection; receptor;
 XX gene therapy.

OS Homo sapiens.

PN WO200263004-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002WO-US003635.

PR 07-FEB-2001; 2001US-0267322P.

PR 23-FEB-2001; 2001US-0271215P.

PR 08-MAR-2001; 2001US-0274551P.

PR 23-MAR-2001; 2001US-0278507P.

PR 30-MAR-2001; 2001US-0280597P.

PR 02-APR-2001; 2001US-0281107P.

PR 06-APR-2001; 2001US-0282121P.

(INCY-) INCYTE GENOMICS INC.

PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG; Hafalia AUA;
 PI Kallikar DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Lu DAM;
 PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
 PI Grail RC, Khan PA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
 PI Warren BA, Yang J, Lee EA, Harland L;

DR WPI; 2002-627557/67.

DR N-PSDB; AAF88585.

PT New human G-protein coupled receptors (GCREC), useful for diagnosing or
 PT treating a disease or condition associated with decreased expression or
 PT over-expression of functional GCRECs e.g. cancer, Alzheimer's and
 PT Parkinson's.

PS Claim 67; Page 166-167; 239pp; English.

XX This invention describes novel polypeptides which have anti-HIV,
 CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,
 CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
 CC antibacterial, fungicide and protozoacide activity. The products of the
 CC invention are useful for treating a disease or condition associated with
 CC decreased expression or over expression of functional G-protein coupled
 CC receptors (GCREC), while antibodies generated against the polypeptide of
 CC the invention are useful for diagnosing a condition or disease associated
 CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
 CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
 CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
 CC The compounds described in the invention can be used for gene therapy.
 CC AAB71327-AAB71369 represent the GCREC proteins encoded by AAF88580-
 CC AAF88627 described in the disclosure of the invention

XX Sequence 367 AA;

Query Match	98.4%;	Score 1610;	DB 5;	Length 367;
Best Local Similarity	99.7%;	Pred. No. 1,2e-171;		
Matches 308;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
OY	5	DEPSMPGHTSNSSCDPIVTPHLLSLVFIYVIGLVGVISLFLVYMMNTRSVTMMVI	64	
DB	59	DEPSMPGHTSNSSCDPIVTPHLLSLVFIYVIGLVGVISLFLVYMMNTRSVTMMVI	118	
OY	65	NLVVHVSVELLVTPRLTYLTKTMMFGLPCKCFVSAMLIHMVTLFFVYVILVTRYLI	124	
DB	119	NLVVHVSFLLVTPRLTYLTKTMMFGLPCKCFVSAMLIHMVTLFFVYVILVTRYLI	178	
OY	125	FPCKDKDKEFYRKLHAAVAASAGMNTLVIVYVPLVVSRYGHEEYNEEHCEPKHELAYT	184	
DB	179	FPCKDKDKEFYRKLHAAVAASAGMNTLVIVYVPLVVSRYGHEEYNEEHCEPKHELAYT	238	
OY	185	YKLIINMIVFVIVAVIILVFOVFITLMWQKRHSLLSHOEWAOLKNLFFIGVILV	244	
DB	239	YKLIINMIVFVIVAVIILVFOVFITLMWQKRHSLLSHOEWAOLKNLFFIGVILV	298	
OY	245	CFLPYQFPRIYVILNVVTHSNACSSKVAFYNEIFLSVTAISCYDLLFFVGGSHMFKOKII	304	
DB	299	CFLPYQFPRIYVILNVVTHSNACNSKVAFYNEIFLSVTAISCYDLLFFVGGSHMFKOKII	358	
OY	305	GLMNCVLCR 313		
DB	359	GLMNCVLCR 367		
RESULT 6				
ID	ADC86555	standard; protein; 448 AA.		
XX	ADC86555;			
XX	AC			
XX	DT	01-JAN-2004 (first entry)		
XX	DE	Human GPCR protein SEQ ID NO:1008.		
XX	KM	human; GPCR; guanosine triphosphate-binding protein coupled receptor;		
XX	KW	gene therapy.		
XX	OS	Homo sapiens.		
XX	PN	EP1270724-A2.		
XX	PD	02-JAN-2003.		
XX	PF	18-JUN-2002; 2002EP-00013517.		
XX	PR	18-JUN-2001; 2001JP-00246789.		
XX	PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.		
XX	PI	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.		
XX	DR	Suwa M, Asai K, Akiyama Y, Aburatani H;		
XX	DR	WPI; 2003-315783/31.		
XX	PS	N-PSDB; ADC86554.		
CC	PT	New polynucleotide, useful for preparing a composition for treating a		
CC	PT	patient in need of increased or suppressed activity or expression of the		
CC	PT	guanosine triphosphate-binding protein coupled receptor.		
CC	PS	Claim 2; SEQ ID NO 1008; 28pp; English.		
CC	CC	The invention relates to a novel polynucleotide encoding a guanosine		
CC	CC	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of		
CC	CC	the invention may have a use in gene therapy. The polynucleotide and		
CC	CC	polypeptide are useful for preparing a composition for treating a patient		
CC	CC	in need of increased or suppressed activity or expression of the		
CC	CC	guanosine triphosphate-binding protein coupled receptor. The protein		

	CC	sequences shown in ADc85549-ADc87617 represent GPCR's of the invention.
	XX	SQ Sequence 448 AA;
	?	
		Query Match 98.4%; Score 1610; DB 7; Length 448; Best Local Similarity 99.7%; Pred. No. 1.ee-17l; Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY		5 DFPSPMGNTSRNNSCDPIVTPHLISLXFIVYLIGGLVGVISILFLVKONTTSVTMAVI 64
Dd		4 DFPSMPGHNTSRNSSCPDITPPLHSLSXFTVLGGLVGVSLIFLLVKONTRSVTTNAVI 63
OY		65 NLVVHVSFELLTVBPRLLTYLIKKTMGELPFCKEFSAMLHHMYLTFLFYVIIIVTRYLI 124
Dd		64 NLYVVHVSFFLLTVPFRLLTYLIKKTMMRGLPFCCKEVSAMLHHMYLTFLFYVIIIVTRYLI 123
OY		125 FPKCKDKVEFKRKAHAVAASAGMTTLVIVVPLVERSGIHEHYNEEHCFKHKELAYT 184
Dd		124 FPKCKDKVEFKRKAAVAASA GMTTLVIVVPLVRSRYGIHEBYNEEHCFKHKELAYT 183
OY		185 YVKLINMIVVFVIAVAVILLVFOVFIMLMVOQLARSSLISHOEFMAOLKNLFPTGYILV 244
Dd		184 YVKLINMIVVFVIAVAVILLVFOVFIMLMVOQLRSHSLSHOEFMALOKNLFFPGIYILV 243
OY		245 CFLPYOFERIIYYLNWVTHSNACKSFAFYNEIPLASVTAISCYDLLFLVFGGSWHFKOXII 304 244 CFLPYOFFRIITYLANVWTHSNACSKSFAFYNEIPLASVTAISCYDLDFVFGSSHWFKOXII 303
OY		305 GLANCVLCR 313 Db 304 GLANCVCRL 312
	RESULT 7	
ID	AAM48989	AAM48989 standard; protein; 305 AA.
AC	XX	AAM48989;
DT	XX	03-MAY-2002 (first entry)
DE	XX	Human testis originated G-protein coupled receptor TGR10.
KW	XX	Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
KW	XX	cyclostatic; immunomodulator; cardiac; neuroprotective; gene therapy;
KW	XX	inflammation; nervous system disease; circulatory system disease; cancer;
KW	XX	metabolic disease; immunological disease; gastrointestinal disease.
OS	XX	Homo sapiens.
PX	XX	WO200196567-A1.
PN	XX	20-DEC-2001.
PP	XX	14-JUN-2001; 2001WO-JP005061.
PR	XX	15-JUN-2000; 2000JP-00184596.
PR	XX	19-JUL-2000; 2000JP-00223887.
PA	XX	(TAKE) TAKEDA CHEM IND LTD.
PI	XX	Moriya T, Ito T, Shintani Y, Miyajima N,
DR	XX	WIJ; 2002-098071/13.
N-	XX	PSDB; AAL44713.
PT	XX	Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat e.g. diseases of central nervous system, inflammations and diseases of circulatory system.
Ps	XX	Claim 1; Fig 2; 11Op; Japanese.
XX		

CC The present invention provides the protein and coding sequences of a
CC novel human testis-originated G protein-coupled receptor protein TGR10.
CC The sequences can be used in the development of drugs for the treatment
CC of diseases of the central nervous system, inflammations, diseases of the
CC circulatory system, cancer, metabolic diseases, immunological diseases,
CC and diseases of the gastrointestinal system. The present sequence is the
CC protein of the invention
XX

SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 5; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.8e-169;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFGHNTSRNSSCDPIVTPHLLISLYFIVLIGGLVGVISILFLVKNNTSVTTMAVINLV 68
DB 1 MFGHNTSRNSSCDPIVTPHLLISLYFIVLIGGLVGVISILFLVKNNTSVTTMAVINLV 60
QY 69 VHSVFLITVFPRLTYLIKKTWFGFLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128
DB 61 VHSVFLITVFPRLTYLIKKTWFGFLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGIHEBYNEHCFFKHKLATYYVKI 188
DB 121 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGIHEBYNEHCFFKHKLATYYVKI 180
QY 189 INVMIVIFVIAVAVILVFOVFIIMLMVOKLRHSLSHOEFPAOLKNLFFIGVILVCFPL 248
DB 181 INVMIVIFVIAVAVILVFOVFIIMLMVOKLRHSLSHOEFPAOLKNLFFIGVILVCFPL 240
QY 249 YQFFRIYILNVVTHSNACSKVAFYNEIFLSTVAISCYDLLFVFGSGHMFQKIIIGLWN 308
DB 241 YQFFRIYILNVVTHSNACSKVAFYNEIFLSTVAISCYDLLFVFGSGHMFQKIIIGLWN 300
QY 309 CYLCR 313
DB 301 CYLCR 305

RESULT 8
AAB71326
ID AAB71326 standard; protein; 305 AA.

AC AAB71326;

DT 19-NOV-2002 (first entry)

DE Human GCRBC-5 INCYTE ID 90012586CD1 SEQ ID 5.

KW GCRBC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW cerebroprotective; antiinflammatory; vinicide; antibacterial; fungicide;
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection; receptor;
KW gene therapy.

OS Homo sapiens.

XX WO200263004-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003635.

XX 07-FEB-2001; 2001US-0267322P.

XX 23-FEB-2001; 2001US-0271215P.

XX 08-MAR-2001; 2001US-0274551P.

XX 23-MAR-2001; 2001US-0278507P.

XX 30-MAR-2001; 2001US-0280597P.

XX 02-APR-2001; 2001US-0281107P.

XX 06-APR-2001; 2001US-0282121P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AR, Walla NK, Arvzu C, Elliott VS, Hafalia AUA;
PI Ramkumar J, Pei J, Tang XT, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan PA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX MPI; 2002-627557/67.
DR N-PSDB; AAF88584.
XX
PT New human G-protein coupled receptors (GCRBC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRBCs e.g. cancer, Alzheimer's and
PT Parkinson's.

Claim 66; Page 165-166; 239pp; English.

CC This invention describes novel polypeptides which have anti-HIV,
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, vinicide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or over expression of functional G-protein coupled
CC receptors (GCRBC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GCRBC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAB71322-AAB71369 represent the GCRBC proteins encoded by AAF88580-
CC AAF88627 described in the disclosure of the invention

SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 5; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.8e-169;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 MFGHNTSRNSSCDPIVTPHLLISLYFIVLIGGLVGVISILFLVKNNTSVTTMAVINLV 68
DB 1 MFGHNTSRNSSCDPIVTPHLLISLYFIVLIGGLVGVISILFLVKNNTSVTTMAVINLV 60
QY 69 VHSVFLITVFPRLTYLIKKTWFGFLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 128
DB 61 VHSVFLITVFPRLTYLIKKTWFGFLPCKFVSAMLIHMVLTFLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGIHEBYNEHCFFKHKLATYYVKI 188
DB 121 KDKVEFYRKLHVAVASAGMWTLYIVVPLVYSRGIHEBYNEHCFFKHKLATYYVKI 180
QY 189 INVMIVIFVIAVAVILVFOVFIIMLMVOKLRHSLSHOEFPAOLKNLFFIGVILVCFPL 248
DB 181 INVMIVIFVIAVAVILVFOVFIIMLMVOKLRHSLSHOEFPAOLKNLFFIGVILVCFPL 240
QY 249 YQFFRIYILNVVTHSNACSKVAFYNEIFLSTVAISCYDLLFVFGSGHMFQKIIIGLWN 308
DB 241 YQFFRIYILNVVTHSNACSKVAFYNEIFLSTVAISCYDLLFVFGSGHMFQKIIIGLWN 300
QY 309 CYLCR 313
DB 301 CYLCR 305

RESULT 9
AAG79446
ID AAG79446 standard; protein; 305 AA.

AC AAG79446;

DT 15-NOV-2002 (first entry)

XX PFI-021.

XX

KM Human; G-protein coupled receptor; GPCR; PFI-021;
 KM peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;
 KM respiratory; neurology; psychology; urogenital disease;
 KM reproductive dysfunction; sexual dysfunction; cancer; tissue repair;
 KM dermatology; skin pigmentation; photocaging; frailty; osteoporosis;
 KM metabolic disease; cardiovascular disease; sleep disorder; hair loss;
 KM gastrointestinal disease; anti-infection; sensory organ disorder.
 XX
 OS Homo sapiens.
 PN EPI225183-A2.
 XX
 PD 24-JUL-2002.
 XX
 PF 09-JAN-2002; 2002EP-00250128.
 XX
 PR 23-JAN-2001; 2001GB-00001739.
 XX
 PA (PFI2) PFIZER LTD.
 PA (PFI2) PFIZER INC.
 XX
 PI Harland L;
 XX
 DR WPI; 2002-601226/65.
 DR N-PSDB; ABA00160.
 XX
 PT New human G-protein coupled receptor involved in signal transduction,
 PT useful to treat disorders associated with its expression or activity such
 PT as inflammation, allergy and cancer.
 XX
 PS Claim 16; Fig 2; 8pp; English.
 XX
 CC This sequence represents a human G-protein coupled receptor (GPCR), PFI-
 CC 021. Expressed sequence tags of the PFI-021 sequence are mainly found in
 CC cDNA libraries from peripheral blood mononuclear cells. Two ESTs have
 CC been identified in libraries derived from breast mRNA. PFI-021 and the
 CC corresponding cDNA are used to treat a patient needing altered activation
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,
 CC neurology, psychology, urogenital disease, reproductive and sexual
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin
 CC pigmentation disorders, photocaging, frailty, osteoporosis, metabolic
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-
 CC infection, sensory organ disorders, sleep disorders and hair loss
 XX
 SQ Sequence 305 AA;
 Query Match 96.9%; Score 1587; DB 5; Length 305;
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 AB004069
 ID AB004069 standard; protein; 305 AA.
 XX
 AC AB004069;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human G protein coupled receptor hrUP29.
 XX
 KM Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
 KM hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37.
 XX
 OS Homo sapiens.
 XX
 PN WO200242461-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-US044386.
 XX
 PR 27-NOV-2000; 2000US-0253404P.
 PR 12-DEC-2000; 2000US-0255366P.
 PR 20-FEB-2001; 2001US-0270266P.
 PR 20-FEB-2001; 2001US-0270286P.
 PR 06-APR-2001; 2001US-0282032P.
 PR 06-APR-2001; 2001US-0282356P.
 PR 06-APR-2001; 2001US-0282358P.
 PR 06-APR-2001; 2001US-0282365P.
 PR 14-MAY-2001; 2001US-0290917P.
 PR 31-JUL-2001; 2001US-0309208P.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX
 DR WPI; 2002-566565/60.
 DR N-PSDB; ABR04867.
 XX
 PT Novel endogenous and non-endogenous versions of G protein-coupled
 PT receptor useful for identification of candidate compounds as receptor
 PT agonists or antagonists for use as therapeutic agents.
 XX
 PS Claim 5; Page 57-58; 84pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC several human G-protein coupled receptors (GPCRs). These can be used in
 CC the identification of candidate compounds as receptor agonists or inverse
 CC agonists having applicability as therapeutic agents. The present sequence
 CC is a GPCR protein of the invention
 XX
 SQ Sequence 305 AA;
 Query Match 96.9%; Score 1587; DB 5; Length 305;
 Best Local Similarity 99.7%; Pred. No. 3.8e-169;
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 240
QY 249 YQFFRIYLYNVVTHSNACSSKVAFYNEIFLSTAIISCYDLLIFVGGSHWPFQKIIIGLMN 308
DB 241 YQFFRIYLYNVVTHSNACNSKVAFYNEIFLSTAIISCYDLLIFVGGSHWPFQKIIIGLMN 300
QY 309 CVLCCR 313
DB 301 CVLCCR 305
RESULT 11
AAU99179
ID AAU99179 standard; protein; 305 AA.
XX AAU99179;
AC 24-SEP-2002 (first entry)
DT Human G protein-coupled receptor IGS70.
XX
DE Human; G protein-coupled receptor; GPCR; IGS70; CNS;
XX Human; G protein-coupled receptor; GPCR; IGS70; CNS;
KW psychiatric disorder; central nervous system disorder; schizophrenia;
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
KW heart failure; angina pectoris; myocardial infarction; kidney disease;
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
KW osteoporosis; allergy.
XX Homo sapiens.
OS
XX MO200244212-A2.
PN 06-JUN-2002.
XX
PD 23-NOV-2001; 2001MO-EP013706.
XX
PF 30-NOV-2000; 2000BP-00204280.
PR 05-DEC-2000; 2000US-0251045P.
XX
PR (SOLV) SOLVAY PHARM BV.
PA
PI Deleersnijder W, Blockx H, De Moor L;
DR MPI: 2002-527703/56.
XX N-PSDB; ABK97351.
DR
XX Novel G-protein coupled receptor IGS70 polypeptide useful for treating
PT dysfunctions, disorders or disease related to lung, bone marrow, spinal
PT cord immune system.
XX
XX Claim 25; Page 7; 58bp; English.
XX
XX The invention relates to a G protein-coupled receptor (GPCR) IGS70
CC polypeptide including sequences that are 98-99.6% identical. Also
CC included are the polynucleotide encoding IGS70 (including sequences 98-
CC 99.6% identical to the polynucleotide or the DNA insert contained in
CC plasmid CBS 109818), a hybridization probe derived from the
CC polynucleotide, a DNA or RNA expression system producing IGS70, a host
CC comprising the expression system, IGS70 receptor membrane preparation
CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is
CC useful for diagnosing a disease or a susceptibility to disease in a
CC subject related to expression or activity of the IGS70 polypeptide in a
CC subject by determining the presence or absence of mutation in the
CC nucleotide sequence encoding IGS70 in the genome of the subject in a
CC sample derived from the subject. IGS70 is also useful identifying agonist
CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified
CC ant/agonists are useful for treating psychiatric and central nervous
CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,
CC multiple sclerosis, anxiety, cardiovascular diseases such as heart
CC failure, angina pectoris, myocardial infarction, kidney disease such as
CC renal failure, gastrointestinal disorders such as irritable bowel

CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
CC inflammation, cancers, asthma, infection (such as bacterial, viral,
CC fungal, protozoal) especially human immunodeficiency virus infection
CC (HIV), diabetes, osteoporosis and allergies. The present sequence
CC represents the human GPCR IGS70
XX
SQ Sequence 305 AA;
Query Match 96.9%; Score 1587; DB 5; Length 305;
Best Local Similarity 99.7%; Pred. No. 3,8e-163;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 MEGHNTSRNSSCDPIVTPHLISLVPFVILIGLVGISILFLVKNKNTSVTTMAVINLV 68
DB 1 MEGHNTSRNSSCDPIVTPHLISLVPFVILIGLVGISILFLVKNKNTSVTTMAVINLV 60
QY 69 VHSVFLTVPPFRLTYLTKTWMFGLPCKFVSAMHIMYLTFLFYVYILVTRYLIFFKC 128
DB 61 VHSVFLTVPPFRLTYLTKTWMFGLPCKFVSAMHIMYLTFLFYVYILVTRYLIFFKC 120
QY 129 KDKVEFRKRLAAVNASAGMWTIVIVVPLVVSRYGHEEVNEBHCFFKELATYTKI 188
DB 121 KDKVEFRKRLAAVNASAGMWTIVIVVPLVVSRYGHEEVNEBHCFFKELATYTKI 180
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 248
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVOKLRHSLSHOEFWAQLKNLFFIGVILVCFLP 240
QY 249 YQFFRIYLYNVVTHSNACSSKVAFYNEIFLSTAIISCYDLLIFVGGSHWPFQKIIIGLMN 308
DB 241 YQFFRIYLYNVVTHSNACNSKVAFYNEIFLSTAIISCYDLLIFVGGSHWPFQKIIIGLMN 300
QY 309 CVLCCR 313
DB 301 CVLCCR 305
RESULT 12
ABP71378
ID ABP71378 standard; protein; 305 AA.
XX
XX ABP71378;
AC
XX 28-APR-2003 (first entry)
DT Human TGR343 protein.
XX
XX
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotoxic;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory.
XX
XX Homo sapiens.
OS
XX WO2003004678-A2.
XX
XX 16-JAN-2003.
XX
XX 01-JUL-2002; 2002MO-US020860.
XX
XX 03-JUL-2001; 2001US-0302800P.
XX
XX (TUL-) TULARIK INC.
PA
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX
XX MPI: 2003-210368/20.
DR N-PSDB; ABZ59171.
XX
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.

XX Claim 17; Page 62; 74pp; English.
PS
XX
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR318 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombinant methodology. The polypeptides are useful for screening or
CC identifying modulators of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR343
CC protein
XX
SQ Sequence 305 AA;
XX
Query Match 96.9%; Score 1587; DB 6; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.8e-169;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 MPEHNTSRNNSCDPIVTPHILISLFFYLIGLVGVISILFLVKNTRSVTTMAVINLVV 68
DB 1 MPEHNTSRNNSCDPIVTPHILISLFFYLIGLVGVISILFLVKNTRSVTTMAVINLVV 60
QY 69 VHSVFLITVPFRLLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFVYVILVTRYLFPKC 128
DB 61 VHSVFLITVPFRLLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFVYVILVTRYLFPKC 120
QY 129 KQVEFFRKLAHVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYTVKI 188
DB 121 KQVEFFRKLAHVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYTVKI 180
QY 189 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGYLVCFPL 248
DB 181 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGYLVCFPL 240
QY 249 YQFFRIYYLVNVTSHNACSKVAFYNEIFLSTVTAISCYDLLLFFVGGSHMFKQKIIGLWN 308
DB 241 YQFFRIYYLVNVTSHNACSKVAFYNEIFLSTVTAISCYDLLLFFVGGSHMFKQKIIGLWN 300
QY 309 CVLCR 313
DB 301 CVLCR 305
RESULT 13
AAO27265
ID AAO27265 standard; protein; 305 AA.
XX
AC AAO27265;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human G-protein coupled receptor GAVE18 protein sequence.
XX
XX Human G-protein coupled receptor; GAVE18; signal transduction;
XX inflammation; physiological immunological response; antiinflammatory;
XX antiasthmatic; antirheumatic; antiarthritic; antisense therapy;
XX chromosomal mapping; tissue typing; forensic biology;
XX predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
XX rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX PN WO2003042399-A2.
XX
XX PD 22-MAY-2003.
XX
XX PF 08-NOV-2002; 2002WO-US035887.
XX

PR 13-NOV-2001; 2001US-0354150P.
PR 22-MAR-2002; 2002GB-00006891.
XX
XX (AVET) AVENTIS PHARM INC.
XX
XX Eshingdrello H, Cai J, Buech SJ, Gassenhuber J;
XX
XX WPI; 2003-457496/43.
DR N-PSDB; AAL57070.
XX
XX New GAVE18 polypeptide and nucleic acid molecule encoding the
PT polypeptide, useful for preventing and treating a disease or disorder
PT associated with aberrant expression or activity of GAVE18, e.g. asthma or
PT rheumatoid arthritis.
XX
XX
PS Claim 7; Fig 6; 88pp; English.
XX
XX This invention relates to a novel G-protein coupled receptor (GAVE18)
CC that is involved in signal transduction in respect to inflammation and
CC the physiological immunological response. Molecules which may modulate
CC the signalling activity or signal transduction of the receptor may be
CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The
CC GAVE18 receptor and the DNA sequence encoding it may be a target for
CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18
CC proteins and antibodies may be useful in screening assays, detection
CC assays (for example chromosomal mapping, tissue typing or forensic
CC biology), or predictive medicine (for example diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics. The
CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse
CC agonist and antagonist are also useful for preventing and treating a
CC disease or disorder associated with aberrant expression or activity of
CC GAVE18, such as inflammation and immunological-related diseases or
CC disorders, for example asthma, chronic obstructive pulmonary disease or
CC rheumatoid arthritis. The present sequence is the amino acid sequence of
CC the GAVE18 protein of the invention
XX
SQ Sequence 305 AA;
XX
Query Match 96.9%; Score 1587; DB 7; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.8e-169;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 MPEHNTSRNNSCDPIVTPHILISLFFYLIGLVGVISILFLVKNTRSVTTMAVINLVV 68
DB 1 MPEHNTSRNNSCDPIVTPHILISLFFYLIGLVGVISILFLVKNTRSVTTMAVINLVV 60
QY 69 VHSVFLITVPFRLLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFVYVILVTRYLFPKC 128
DB 61 VHSVFLITVPFRLLTYLIKKTMMFGLPFCFVSAMLIHMVLTFLFVYVILVTRYLFPKC 120
QY 129 KQVEFFRKLAHVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYTVKI 188
DB 121 KQVEFFRKLAHVAASAGMTLVIVVPLVSRVYGHSEYNEBHCFFKHELAATYTVKI 180
QY 189 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGYLVCFPL 248
DB 181 INMYIVFVIAVAIVLIVPQVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGYLVCFPL 240
QY 249 YQFFRIYYLVNVTSHNACSKVAFYNEIFLSTVTAISCYDLLLFFVGGSHMFKQKIIGLWN 308
DB 241 YQFFRIYYLVNVTSHNACSKVAFYNEIFLSTVTAISCYDLLLFFVGGSHMFKQKIIGLWN 300
QY 309 CVLCR 313
DB 301 CVLCR 305
RESULT 14
ADB78590
ID ADB78590 standard; protein; 305 AA.
XX
XX ADB78590;
XX

DT	04-DEC-2003	(first entry)
XX		
DE	Human G-protein coupled receptor GAVE18.	
XX		
KW	human; GAVE19 orthologue; G-protein coupled receptor; GAVE18;	
XX	inflammatory disorder; immunological disorder.	
OS	Homo sapiens.	
PN	WO2003068803-A2.	
XX		
PD	21-AUG-2003.	
XX		
PF	13-FEB-2003; 2003WO-US004350.	
XX		
PR	14-FEB-2002; 2002US-0356686P.	
XX	22-AUG-2002; 2002GB-00019574.	
PA	(AVET) AVENTIS PHARM INC.	
XX		
PI	Eishngdrello H, Dressler H, Cai J, Wright P;	
XX		
DR	WPI; 2003-646474/61.	
PT	New GAVE19 gene, useful for preparing a composition for treating	
PT	inflammatory or immunological disorders.	
XX		
XS	Example 1; Fig 4; 76pp; English.	
XX		
CC	The invention comprises the amino acid and coding sequence of the mouse	
CC	GAVE19 protein. Mouse GAVE19 is a G-protein coupled receptor which is the	
CC	orthologue of human GAVE18. The DNA and protein sequences of the	
CC	invention are useful for treating inflammatory and immunological	
CC	disorders. The present amino acid sequence represents the human GAVE18	
XX	protein.	
SQ	Sequence 305 AA;	
XX		

	Query Match	96.9%	Score 1587	DB 7	Length 305
	Best Local Similarity	99.7%	Pred. No. 3.8e-169		
	Matches 304	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY	MPGHNTSNSSCDPIVTPHLLISLYEIVLIGGIWGVISILFLIVKNTKRSVTTMAVINLV	68			
DB	1 MPGHNTSNSSCDPIVTPHLLISLYEIVLIGGIWGVISILFLIVKNTKRSVTTMAVINLV	60			
QY	69 VHSVFLVVPRLITLTKTMMFGLPCKCFYSAMAHIMYLTFLFYVYLITRYLIFPKC	128			
DB	61 VHSVFLVVPRLITLTKTMMFGLPCKCFYSAMAHIMYLTFLFYVYLITRYLIFPKC	120			
QY	129 KDKEFYRKLAHVAASAGMTLVIVTVPLVVSRYGHEEYNEEHCFFKHKLATTVYKI	188			
DB	121 KDKEFYRKLAHVAASAGMTLVIVTVPLVVSRYGHEEYNEEHCFFKHKLATTVYKI	180			
QY	189 INIMVIVVIAVAVLLVFOVFIIMLMOQKLRHSLSHOEFWAOLKTLPTIGVILVCELP	248			
DB	181 INIMVIVVIAVAVLLVFOVFIIMLMOQKLRHSLSHOEFWAOLKTLPTIGVILVCELP	240			
QY	249 YQFFRIYYLVNTVTHSNACKSKAIFYNEITFLSVTAISCDLLEFVGGSHWPKOKIIGLMM	308			
DB	241 YQFFRIYYLVNTVTHSNACKSKAIFYNEITFLSVTAISCDLLEFVGGSHWPKOKIIGLMM	300			
QY	309 CVLGR 313				
DB	301 CVLGR 305				

RESULT 15

AD028918

AD028918 standard; protein; 305 AA.

XX AD028918;

29-JUL-2004 (first entry)

Human novel GPCR PGR13, SEQ ID NO:17.

G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiParkinsonian; antiemic; cytosstatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antihistoidal; antianaemic; antiseboic; dermatological; antitumor; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; receptor.

Homo sapiens.

WO200404000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-040903P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F, Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H; WPI; 2004-390329/36.

N-PSDB; ADO28919.

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 1; SEQ ID NO 17; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the

CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 305 AA;

Query Match 96.9%; Score 1587; DB 8; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.8e-169;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	9	MPGHNTSRNSSCDPIVTPHLISLYFIYVILGGLVGVISILFLLVMQNTRSVTTMAVINLAV	68
Db	1	MPGHNTSRNSSCDPIVTPHLISLYFIYVILGGLVGVISILFLLVMQNTRSVTTMAVINLAV	60
Qy	69	VHSVFLLTVPFRLTYLLIKKTMMFGLPFCFVSAMLHIMYLTFLFYVVLVTRYLIPEKC	128
Db	61	VHSVFLLTVPFRLTYLLIKKTMMFGLPFCFVSAMLHIMYLTFLFYVVLVTRYLIPEKC	120
Qy	129	KDKVEFYRKLHAAVAAAGMTLVIVIVPLVVSRYGIHEBYNEBHCPEHKELAYTYVKI	188
Db	121	KDKVEFYRKLHAAVAAAGMTLVIVIVPLVVSRYGIHEBYNEBHCPEHKELAYTYVKI	180
Qy	189	INTMIVIFVLAVALIILVFOVFIIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCELP	248
Db	181	INTMIVIFVLAVALIILVFOVFIIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILVCELP	240
Qy	249	YQFFRIYYLNVVTHSNACSSKVAFYNEIFLSVTAISCYDILLFVFGSHWFKOKIIGLMN	308
Db	241	YQFFRIYYLNVVTHSNACSSKVAFYNEIFLSVTAISCYDILLFVFGSHWFKOKIIGLMN	300
Qy	309	CVLCR 313	
Db	301	CVLCR 305	

Search completed: September 10, 2005, 10:07:03
Job time : 82 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 10:03:32 ; Search time 23 Seconds

(without alignments)
1309.385 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637

Sequence: 1 MQGCDPSPMGHNTSRNSC.....GSHWFKQKTIIGLNCVLCR 313

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	13.6	391	A39297	somatostatin recep
2	221	13.5	391	A41795	somatostatin recep
3	221	13.5	391	C41795	somatostatin recep
4	220	13.4	344	T09508	inturin 17 purinerg
5	214	13.1	328	I38973	G protein-coupled
6	208	12.7	355	A55733	G protein-coupled
7	207.5	12.7	355	A45177	chemokine (C-C) re
8	207.5	12.7	356	I49340	MIP-1 alpha recept
9	206	12.6	369	JC2083	somatostatin recep
10	206	12.6	369	D41795	somatostatin recep
11	205	12.5	369	B41795	somatostatin recep
12	205	12.5	369	A45291	somatostatin recep
13	203	12.4	346	S29288	somatostatin recep
14	202.5	12.4	432	A43448	thrombin receptor
15	202	12.3	355	I49339	macrophage inflamm
16	201.5	12.3	308	I50241	G protein-coupled
17	201.5	12.3	420	I51667	thrombin receptor
18	199	12.2	355	JQ1231	interleukin-8 rece
19	198.5	12.1	370	JC5549	heptahelical P2Y5-
20	197.5	12.1	380	JC2338	kappa opioid recep
21	197.5	12.1	384	A47249	brain-specific som
22	196	12.0	425	A37912	thrombin receptor
23	196	12.0	428	A44021	somatostatin recep
24	195	11.9	362	S33733	G protein-coupled
25	194.5	11.9	380	JC2434	kappa opioid recep
26	194	11.9	355	JC04304	orphan G protein-c
27	194	11.9	388	JN0605	somatostatin recep
28	193.5	11.8	367	JC2421	opioid receptor ho
29	193.5	11.8	367	I49022	kappa opioid recep

30	193.5	11.8	367	2	I56520	G protein-coupled
31	193	11.8	355	2	JC5067	G protein-coupled
32	193	11.8	380	2	A55259	kappa opioid recep
33	192.5	11.8	355	2	G02436	chemokine (C-C) re
34	192	11.7	370	2	S43087	orphan opioid rece
35	191.5	11.7	380	2	A48227	kappa opioid recep
36	191.5	11.7	428	2	S30508	probable G protein
37	191	11.7	380	2	S36143	kappa opioid recep
38	190.5	11.6	384	2	JC4629	somatostatin recep
39	190.5	11.6	423	2	JC7677	allatostatin recep
40	189.5	11.6	333	2	I38974	G protein-coupled
41	189	11.5	373	2	JEB087	delta opioid recep
42	186	11.4	418	2	A46226	somatostatin recep
43	185.5	11.3	383	2	S55594	G protein-coupled
44	185	11.3	400	2	I56553	mu opiate receptor
45	184	11.2	392	2	S65693	opioid receptor mu

ALIGNMENTS

RESULT 1

A39297

somatostatin receptor - rat

N;Alternate names: probable G-protein-coupled receptor; SRIF receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004

C;Accession: A39297; A45102; S20088

R;Meyerhof, W.; Pautz, H.U.; Schoenrock, C.; Richter, D.

DNA Cell Biol. 10, 689-694, 1991

A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor express.

A;Reference number: A39297; MIMD:92096119; PMID:161599

A;Accession: A39297

A;Molecule type: mRNA

A;Residues: 1-391 <MEY>

A;Cross-references: UNIPROT:P28646; GB:X62314; GB:X61630; NID:G56309; PIDN:CAA44193.1; i

A;Experimental source: brain

A;Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated

R;Li, X.J.; Forte, M.; North, R.A.; Rose, C.A.; Snyder, S.H.

J. Biol. Chem. 267, 21307-21312, 1992

A;Title: Cloning and expression of a rat somatostatin receptor enriched in brain.

A;Reference number: A45102; MIMD:93016064; PMID:1400442

A;Accession: A45102

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-391 <Li1>

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBI:P:116692)

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 13.6%; Score 222; DB 2; Length 391;

Best Local Similarity 22.8%; Pred. No. 8e-11;

Matches 72; Conservative 75; Mismatches 119; Indels 50; Gaps 14;

QY	10	PGHNTSRNS-CDPIVTPHLIS-LPFIYLIGLVG--VISLFLVKNRNSVTTMAVI	64
DB	41	PGHNSQNGTLSEGGQSALISFIYSVCLVAGCGSNWIVYILRAYAKKT--ATNIYIL	98
QY	65	NLVVHVSFLLVTPFPLTLTIKKTMFGLPCKFPYSAAMHIMYILFLVYVILVTRYL	124
DB	99	NLAIDELMLSPFLVISTLIRHWFGLDRLVLDVAVMFYSITCLTVLSDVRVA	158
QY	125	FFCKDKVEFYRKLHVAASAGMTLVIVVPLV-STRGIEEYNEBCEFKHELAY	183
DB	159	VHPIAARVRRPTAKVNVNLGVWLSLIVLPVFESTANS-GLYACMMLEPPO	217
QY	184	TY-VKLTINMIV-FVIAVAVILLVQVETIMLWQKLSHLSHOEFAQIKN-----	235
DB	218	RMLVGFVLTFLMGLFPLVGAICLCY-----VLIIAKNR--NVALKAGQGRSEBRKT	270
QY	236	---LPIGIVLVCPLPYQFRIVYLVN-----VTHSNACSSKVAF-----	272

Db		271	LMAVVAVVVFVICMMP--FYVVQLVNVAEODDATVQGLSVILGIVANSKANPILYGFSLD	328
Oy		273	-YNELFISVTATSCYD	287
	:	:	:	:
Db		329	NFKRSFORILCLSWMD	344

RESULT 2

```

A41795
somatostatin receptor 1 - human
C|Species: Homo sapiens (man)
C|Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C|Accession: A41795
R|Yamada, Y.; Post, S.R.; Mang, K.; Tager, H.S.; Bell, G.I.; Selino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A|Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors.
A|Reference numbers: A41795; MUID:92108031; PMID:1346068
A|Accession type: DNA
A|Molecule type: DNA
A|Residues: 1-391 <YAM>
A|Cross-references: UNIPROT:P30872; GB:M81829; NID:G307433; PIDN:AAA58247.1; PID:G307433
A|Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIPI:74768)
C|GeneID:8
A|Gene: GDB:SSTR1
A|Cross-references: GDB:134185; OMIM:182451
A|Map position: 14q13-14q13
A|Introns: #status absent
C|Superfamily: vertebrate rhodopsin
C|Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pnc
F|58-84/Domain: transmembrane #status predicted <TM1>
F|95-120/Domain: transmembrane #status predicted <TM2>
F|133-153/Domain: transmembrane #status predicted <TM3>
F|173-195/Domain: transmembrane #status predicted <TM4>
F|220-250/Domain: transmembrane #status predicted <TM5>
F|269-296/Domain: transmembrane #status predicted <TM6>
F|307-336/Domain: transmembrane #status predicted <TM7>
F|44,44,48,381/Binding site: carboxylate (Asn) #status predicted
F|130-208/Disulfide bonds: #status predicted
F|172/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted
F|265/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
F|339/Binding site: palmitate (Cys) (covalent) #status predicted

```

Query Match	13.5*	Score 221;	DB 2;	Length 391;
Best Local Similarity	22.8*	Pred. No. 9.6e-11;		
Matches	%	Conservative	74;	Mismatches 120; Indels 50; Gaps 14;
Oy		10	PGHNTSRNS--CDPIVTEPHLIS-LYFIVLIGLVG---VISILFLVMKTRSTWTMAVI	64
	:	:	:	:
Db		41	PNRAASQNGTLSEGGSGAILISFISVVCIVAGLGNSMVIVILIRAKMKI--ATNIYL	98
Oy		65	NLVNVHSFLLTVPRRLTYLIKTTMGEGLPCKFVSAMLHMTLTFLFYVILIITYRLI	124
	:	:	:	:
Db		99	NLAIADELMLMSVPFLVYSTLRHPFGALLCRVLSDVANMMETSIFYCLVLVSDRYVA	158
Oy		125	FFKKDKVEFRKLAAVVASAGMWTLVVIIVPLV--SRYGIEHYNEEHCFKHKELAY	183
	:	:	:	:
Db		159	VNHPIKARYRRPYPAKVKNIGWNLSTLVLIPIVBSRTKAND--GVACNMIMPBAQ	217
Oy		184	TY-VKIINMYTI-VFIAVAVILLVFOVFTIMAVOKLRSHLSHQEFMAOLKN-----	235
	:	:	:	:
Db		218	RMLVGFWLYTFLMGELLFEVGAICLY-----VLIIRKMR--MVALKGMQQRKRSEKIT	270
Oy		236	--LFFIGVILLVCPFLPYOFPRIYYLN-----VHNSNACSKVAF-----	272
	:	:	:	:
Db		271	LMVNNVNVWFVICMMP--FYVVQLVNVAEODDATVQSLSVILGYANSCANPILYGFSLD	328
Oy		273	-YNELFISVTATSCYD	287
	:	:	:	:
Db		329	NFKRSFORILCLSWMD	344

RESULT 3
 A41795

somatostatin receptor 1 - mouse

C|Species: Mus musculus (house mouse)
C|Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C|Accession: C41795
R|Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A|Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
A|Reference number: A41795; MUID:92108031; PMID:1346068
A|Accession: C41795
A|Status: nucleic acid sequence not shown
A|Molecule type: DNA
A|Residues: 1-391 <YAM>
A|Cross-references: UNIPROT:P30873; GB:M81831; NID:g201058; PIDN:AAA8255.1; PID:g201058
C|Superfamily: vertebrate rhodopsin
C|Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 13.5%; Score 221; DB 2; Length 391;
Best Local Similarity 22.8%; Pred. No. 9.6e-11;
Matches 72; Conservative 74; Mismatches 120; Indels 50; Gaps 14;

Oy 10 PGNHTSNSS-CDPITVPHLIS-LYFVLIGLVG--VSILFLVKMTTSVTMAVI 64
|||::||::||::||::||::||::||::||::||::||::||::||::||
Db 41 PGRRAOUGTLSEGGSAIILISFYVCLVGLCGNSMIVYLIRAKMTT--ATNIYIL 98
65 NLVVHVSFLLYTFEPLTYLLIKRTMGELPCKCFVASMLIHMYLTFLFYVILLTRYLI 124
Oy 99 NLAIADLELMISVFVLTSTLRHMFGALLCRVLTVSDVANMETSICYCTLVSVDRYA 158
Db 125 FFKKDKVEFRKLHAANAAGMWTLVIVIVLPVLS-SRGIHENYNEHCFFHEKELAY 183
Oy 159 VHDPIKARRRPFTVAAVVMVGWVLSLVLLPLVFSKRPAASD-GTVA CNMIMPEPAQ 217
Db 184 TV-VKIINMIIVL-FVIAVAVILLVPEQFETIMLVQKLRHSLSHOEFMAQLKN----- 235
Oy 218 RMLVGFVLYTEFMGFLPLPVGALICCY-----VIIAGMR--TWALKKGWGQRKRSEKIT 270
Db 236 ---LFPLGVLLCPYPQFPRIYYLANV-----VTHSACSSKAFA----- 272
Oy 271 LMMWMVVMVFWVICMP--FVVVOLVNVPABODDATVSQLSVIIYGANSKANPILDYGLSD 328
Db 273 -YNEIFLSVTAISCYD 287
Oy 329 NFKRSPFORICLSMMD 344
Db

RESULT 4
T09508
Intron 17 putative receptor P2Y5 - human
N|Alternate names: G-protein coupled receptor
C|Species: Homo sapiens (man)
C|Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C|Accession: T09508
R|Bohm, S.K.; Trumpff, A.; Khitri, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A|Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinol
A|Reference number: Z16705
A|Accession: T09508
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: mRNA
A|Residues: 1-344 <BOH>
A|Cross-references: UNIPROT:P43657; EMBL:A000546; NID:g2232068; PID:g2232069
C|Genetics:
A|Map position: 13
C|Superfamily: ATP receptor P2U
C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match 13.4%; Score 220; DB 2; Length 344;
Best Local Similarity 27.4%; Pred. No. 1e-10;
Matches 76; Conservative 53; Mismatches 128; Indels 20; Gaps 12;

Oy 31 LYFVLIGLV-LVISLFLVKNTRSYTTMAVINLVVHVSFLLTVPRLLTYLIKKTW 89
:::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 23 MFMSVFLGLVSNCAIYIFICVLKVENETTYMINIAMSDLFEVPTLPRIIFYTTRNW 82

QY 90 MFGLPCKEVSAMLIHMYLTFELFYVILVTRYL-IPKCKDKVEFYRKLHVAASAAGMW 148
 DB 83 PFGGLLCKISVMTLYTMTWIGSLITLCTISVDFALIVPEFSKL-LTKRNAAKVCCTGVW 141
 QY 149 TLVIVIVPLVSVRYGHEBYN--EEHCFKFKELAY-TYVKINIMVIFVIAVAAIL- 204
 DB 142 LTVIGSAPAVFVQ-STHSQGNNASEACFENFPEATWKTYS----RIVIFELVGFIP 196
 QY 205 LVFQVFIIMLVQCLRSL-LSHQEF-MAQKLNFPFGVIL--VCLPYPQCFRIYYIANV 260
 DB 197 LILAVTSSMWLTKLTPVTLISREKINKTKVLMKMFHLLIFCFQFVPYINILILYSIVR 256
 QY 261 THSNACSSKVAFYNEIFLSTVAIS----CYDLLLFFV 293
 DB 257 TQTFVNCSSVANAATMTPTITCLIVSNCCFDPVIYVF 293

RESULT 5

138973
 G protein-coupled receptor 7 - human
 C/Species: Homo sapiens (man)
 C/Date: 24-May-1996 #sequence revision 24-May-1996 #text_change 09-Jul-2004
 C/Accession: J38973
 R/O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
 Genomics 28, 84-91, 1995
 A/Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
 A/Reference number: A57647; MUID:96070436; PMID:7590751
 A/Accession: J38973
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-328 <RES>
 A/Cross-references: UNIPROT:P46145; EMBL:U22491; NID:g953232; PIDN:AAC50197.1; PID:g9532
 C/Genetics:
 A/Gene: GDB:GPR7
 A/Cross-references: GDB:371714; OMIM:600730
 A/Map position: 10q11.2-10q21.1
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 13.1%; Score 214; DB 2; Length 328;
 Best Local Similarity 21.2%; Pred. No. 3.1e-10;
 Matches 61; Conservative 66; Mismatches 125; Indels 36; Gaps 9;

QY 10 PCHNTSNSSCDPIVTPHLIS--LYFVLIGLVGISILFLVKN-NTRSVTMAVIN 65
 DB 19 PALSCSNASTLAPAPLAVAVPVYAVVICAIVGAGNSAVLYVLLRAPRMKVTNLFIIN 78
 QY 66 LVVHVSFLTLVPEPLTYLTKTWMFGLPCKEVSAMLIHMYLTFEYVILVTRYLIF 125
 DB 79 LAIADELFTVLPLINADFLIRQMPFELMKCLIVAIIDQYNTSSLYFLTVMGADRLV 138
 QY 126 FKCKDKVEFYRKLH--AFAASAGMTLVIVIVPLVSVRYGHEBYNEHC-FKFKELA 182
 DB 139 LATAESRRVAGRTYSABAVSLAVWGIVTLVLPFAVFA-RLDDQGRQCVLVFPPEA 197
 QY 183 YTVVKIINIVIV-FVIAVAVILLVFOVFIIMLVQCLRSLLSHQEFMAQKLN----- 235
 DB 198 FMRASRLTYLVIFALPVESTICVLYTTLICRLHAKMLD---SHAALTRAKKRVTV 253
 QY 236 LVFQVFIIMLVQCLRSLLSHQEFMAQKLN-----YLANVVTSHSNAC 266
 DB 254 VALIAVCLLCMTYHSTVALTTDLFQPLVIAISITSLYVANS 301

RESULT 6

A55733
 G protein-coupled receptor GPR1 - human
 C/Species: Homo sapiens (man)
 C/Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
 C/Accession: A55733
 R/Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Taut, I
 Genomics 23, 609-618, 1994

A/Title: Cloning of human genes encoding novel G protein-coupled receptors.
 A/Reference number: A55733; MUID:95154831; PMID:7851889
 A/Accession: A55733
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-355 <MAR>
 A/Cross-references: UNIPROT:P46091; GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g57741
 C/Genetics:
 A/Gene: GDB:GPR1
 A/Cross-references: GDB:371707; OMIM:600239
 A/Map position: 15q25-15q26.1
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 12.7%; Score 208; DB 2; Length 355;
 Best Local Similarity 25.4%; Pred. No. 1e-09;
 Matches 77; Conservative 53; Mismatches 101; Indels 72; Gaps 15;

QY 27 HLIS--LYFVLIGLVG-VISILFLVKNTRSVTMAVINLVVHVSFLTLVPEPLTY 83
 DB 38 HWVSLVLYCIAFVLGIPGNAIVWFTGLKWK-KTVITLWFLNALADFLFLPLVISTY 96
 QY 84 L-IKTWMFGLPCKEVSAMLIHMYLTFEYVILVTRYLIFPKCKDKVEFYRKLHVA 142
 DB 97 VANNFMRPQIWCXANSFTQAQMFASVPELVISLDHY-----HLHPVL 144
 QY 143 ASAGMW--TLVIVIVPLVSVRYGHEBY-----NEHC--FKFH-----KEL 181
 DB 145 SHRRRLKNSLIVIFITWILASLIGPALYFRDVEFNHTLCYNNFQKHPDLTLIRH 204
 QY 182 AATYVK-IINVMVIVIAVAIVLVFQVFIIMLVQCLRSLLSHQEFMAQKLNFPFG 240
 DB 205 VLVWVFPIIGYLPPLTMSCYCLIFKV-----KRTVLISSRHFWT--LIVVV 253
 QY 241 VLVCELPYQFRIYIVAVVTHSNACSSKY-----AFYNEIFLSTVAISCYDLL 289
 DB 254 AFVVCMTPTPLPFIWELTI--HNSYSHVMQAGIFLSTGLARLN-----SCLNPI 302
 QY 290 LFV 292
 DB 303 LVV 305

RESULT 7

A45177
 chemokine (C-C) receptor 1 - human
 N/Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: A45177; 155671
 R/Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A/Title: Molecular cloning, functional expression, and signaling characteristics of a C
 A/Reference number: A45177; MUID:93161416; PMID:7679328
 A/Accession: A45177
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-355 <NEO>
 A/Cross-references: UNIPROT:P32246; GB:U10918; NID:g292416; PIDN:AAA36543.1; PID:g29241,
 A/Note: sequence extracted from NCBI backbone (NCBI:P.124876)
 R/Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A/Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A/Reference number: 155671; MUID:93240122; PMID:7683036
 A/Accession: 155671
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-355 <RES>
 A/Cross-references: GB:U10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C/Genetics:
 A/Gene: GDB:CMKBR1; CMK-1
 A/Cross-references: GDB:138446; OMIM:601159

FT NON TER 1 1
 FT NON TER 152 152
 SQ SEQUENCE 152 AA; 18091 MW; B6B146A57EC7582 CRC64;
 Query Match 48.1%; Score 787; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.1e-42;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 76 TVPRRLVYLTKCTMFGLPCKFVSAMLHIMYLTLPYVYLITRLLIPKCKOKYEFY 135
 DB 1 TVPRRLVYLTKCTMFGLPCKFVSAMLHIMYLTLPYVYLITRLLIPKCKOKYEFY 60
 QY 136 RKLHVAASAGMTLVIVVPLVVSXRGHIEENECHECFKELAYTYKLIINMIVI 195
 DB 61 RKLHVAASAGMTLVIVVPLVVSXRGHIEENECHECFKELAYTYKLIINMIVI 120
 QY 196 FVIAVAVILLVQVFIIMLVQKLRHSLSHQ 227
 DB 121 FVIAVAVILLVQVFIIMLVQKLRHSLSHQ 152
 RESULT 5
 Q80UC5 PRELIMINARY; PRT; 131 AA.
 ID Q80UC5;
 AC Q80UC5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE G-protein-coupled receptor POR13 (Fragment).
 GN Name=Gpr141;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX SEQUENCE FROM N.A.
 RP MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
 RA Vasiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.B.,
 RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
 RA Bergman J.B., Galanakis G.A.;
 RT "The G-protein-coupled receptor repertoire of human and mouse.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).
 DR EMBL; AY255553; AAC85065.1; -
 DR MGD; MGI:2672983; Gpr141.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON TER 1 1
 FT NON TER 131 131
 SQ SEQUENCE 131 AA; 15261 MW; 58089C0AF5490DE1 CRC64;
 Query Match 33.4%; Score 547; DB 2; Length 131;
 Best Local Similarity 78.7%; Pred. No. 1.5e-27;
 Matches 100; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 QY 186 VKIINMIVFVAVAVVILVQVFIIMLVQKLRHSLSHQEFMQLKYLFIIGVILVC 245
 DB 5 VKIINMIVFVAVAVVILVQVFIIMLVQKLRHSLSHQEFMQLKYLFIIGVILVC 64
 QY 246 FLFYPQFRIRYLVNVVTHSNACSSKVAFYNEIFLVTVAISCYDILLFVFGSHWFKQKITG 305
 DB 65 FLFYPQFRIRYLVNVVTHSNACSSKVAFYNEIFLVTVAISCYDILLFVFGSHWFKQKITG 124
 QY 306 LAMCVLC 312
 DB 125 MAMCLLC 131
 RESULT 6
 Q8BLT7 PRELIMINARY; PRT; 299 AA.
 ID Q8BLT7;
 AC Q8BLT7;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
 DE enriched library, clone:A530095019 product:hypothetical Rhodopsin-like
 DE GPCR superfamily containing protein, full insert sequence.
 GN Name=A530095019Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6679(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Niehi K., Kitsuami T., Taahiro H., Itoh M.,
 RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Tameda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:11757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa T., Kaishwagi K.,
 RA Kato H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK041317; BAC30904.1; -
 DR MGD; MGI:2441809; A530095019Rik.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

DR GO:0007186; P;G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro: IPR000276; GPCR Rhodopsn.
DR InterPro: IPR002286; P2_purinocptr.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 299 AA; 34594 MW; D793823AF030E67D CRC64;

Query Match 32.5%; Score 532; DB 2; Length 299;
Best Local Similarity 37.1%; Pred. No.2.5e-26;
Matches 104; Conservative 66; Mismatches 104; Indels 6; Gaps 4;

QY 20 CDPIVPHLISLVFIYVIGLVGVISILFLVYKNTSRVYTMVAVINLVVHVSFLLTVPF 79
DB CDHCAKAILTTAVSVFPGVGTVMHSHMFKRNCQSMIATIIINIVHSLILSLF 83
QY 80 RLTYLIKTYMFGLPCKFVSAMLIHMYITFLFYVILVTRYLIFPKCKDKVEFRKLI 139
DB RLSTYSAVWKGSFTCRWVSGVYGHMYITFLFYVAVTLRLIYFK-KLQMOQLQKH 142
QY 140 AVAASAGMNTLVIVVPLVSVRYGHEEYNE-EHCFKHKLATYTVKINMVIYFI 198
DB AVALSTIIIVTGSFTLPIFLFYGTDPSTTEQQRCEFRKSLNSRDIIINISIIIVIM 202
QY 199 AVAVILVFOVFIIMLVQKLRHSLSHOEFMVQKLNLFPIGVILVCPYQFRIYYP- 257
DB TTYLLFLQMAVILHLIKAYWPDMAHGEYRQIKSPFFLVIYVCFIPHAFRVYFIQ 262
QY 258 NVVTHSNACSSKVAFNEIFLSTVTAISCYDLLIFVFGSH 297
DB NPPEQEN---SKLIYNEICVALTACDMLCFIGGVII 299

RESULT 7

ID 06XCE1 PRELIMINARY; PRT; 381 AA.
AC 06XCE1;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE G-protein-coupled receptor GPR34.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
R4 MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;
RA Schultz A., Schoneberg T.;
RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";
RL J. Biol. Chem. 278:35531-35541(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY241090; AAP0429.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002286; P2_purinocptr.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 381 AA; 43619 MW; E0837BA1FD29666A CRC64;

Query Match 16.9%; Score 277; DB 2; Length 381;
Best Local Similarity 25.7%; Pred. No.4.2e-10;
Matches 81; Conservative 73; Mismatches 137; Indels 24; Gaps 11;

QY 14 TERNSSC---DPIVPHLISLVFIYVIGLVGVISILFLVYKNTSRVYTMVAVINLVV 69
DB TORANCFLEDNALSFALISFYSVIFVIGLVGNITALEAFCLCHKRSIQVLLNVAIA 91
QY 70 HSVFLTVFPRLLTYLI-KTYMFGLPCKFVSAMLIHMYITFLFYVILVTRYLIFPKC 128
DB DLLIFCLPFRILYHISNNWFMGWLICKIVGTLEFYNNYISILLGISLDRYKINS 151
QY 129 KDKVEFRKLIHVAASAGMNTLVIVVPLVSVRYGHEEYNEHCFKHKLAVT 184
DB VKRPKMLTTTSRVHICCIWMAVALGFSLVVPSLFR---SDISNSTLCFHYRNKQAM 207
QY 185 YKINIMYIVFVIAVAAILVFOVFII--MLMVQKLRHSLSHOEFMVQKLNLFPIGV 242
DB TEALINMYIIVMFVVPFLILLISYKIAKNLKSIRKANFPNAYKQYOTARNSFIVLI 267
QY 243 L-VCELPYQFRIYVILNVVTHSNACSSKVAFY--NEIFLSTVTAISCYDLLIFVFGSHW 298
DB FTVCFFVPMFREFVYITSQIQNPSCYWKGIHHTCNVMLIFSSFNSCIDPVWY-FLMESS 326
QY 299 FKQKIIGLMNCVLCR 313
DB 327 VAKTVLQI---ICR 337

RESULT 8

ID 06XCB2 PRELIMINARY; PRT; 378 AA.
AC 06XCB2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE G-protein-coupled receptor GPR4 type 1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;
RN [1]
RP SEQUENCE FROM N.A.
R4 MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;
RA Schultz A., Schoneberg T.;
RT "The structural evolution of a P2Y-like G-protein-coupled receptor.";
RL J. Biol. Chem. 278:35531-35541(2003).
CC EMBL; AY241119; AAP04328.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0045028; F:purinergic nucleotide receptor activity; G. . .; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002286; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 378 AA; 42747 MW; 988071FD3483A86 CRC64;

Query Match 16.0%; Score 262; DB 2; Length 378;
Best Local Similarity 28.9%; Pred. No.3.7e-09;
Matches 90; Conservative 62; Mismatches 133; Indels 26; Gaps 14;

QY 7 PMPGHNTSRNSSC---DPIVPHLISLVFIYVIGLVGVISILFLVYKNTSRVYTMVAV 63
DB PSTBPH-INHSQCHQEDENLRPLAAYSLPFVFLVGNLALAWFLQRRSSNNLRFL 72
QY 64 INLVVHVSFLLTVPPRLTY-LIKTYMFGLPCKFVSAMLIHMYITFLFYVILVTRY 122
DB INCAVADVLLGLCLPFRISYHNLGDMHIGPLACKMGVNLFYNNYISIMLGFISLHY 132

QY 123 LIFEKCD-----KVEFYRKLHAAVAAAGMTLVIVVPLVSVRGHIEYNEHC 174
DB 133 L-RIKGGRAROGITVTLGLGRCPWSVACGTMISLVLGVPMIVN---AEDEHSNKC 188
QY 175 EKFEKELAYTVYK-IINMIVIFVIAVAVILLVFOVELI--MLMVQKLRHSLSHQEFMA 231
DB 189 FQFMGRSGNGKGAIFVVLVFPFVLMVSVYVIAKSLRLVSDKDLPRNAHYOR 248
QY 232 QLNLFPI-GVILVCLPYOFR-IYYLVNVTSHNACS--SKVAFNEIFLSTVTAI-SCY 286
DB 249 SAKSFFVLFLFVFCFPHYAFRPVYIFYOIKNNQPCBIIQMVARTNEIMLLSAFNSCL 308
QY 287 D-LILFVFGCS 296
DB 309 DPVWYFLLSGS 319
RESULT 9
Q6XCES
ID Q6XCES PRELIMINARY; PRT; 359 AA.
AC Q6XCES;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G-protein-coupled receptor GPR34 (Fragment).
OS Martes foina (Beach marten).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Martes.
OX NCBI_TaxID=9659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22841141; PubMed=12835326; DOI=10.1074/jbc.M303346200;
RA Schulz A., Schoneberg T.;
RT "The structural evolution of a P2Y-like G-protein-coupled receptor."
RL J. Biol. Chem. 278:35531-35541(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AY241086; AARP04295.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR002286; P2_purinocptor.
DR Pfam: PF00001; 7tm.1; 1-
DR PRINTS: PRO0237; GPCRHOOPSN.
DR PRINTS: PRO1157; P2YPRNOCPTR.
DR PROSITE: PS00237; G_PROTEIN_RECBP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECBP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 359
SQ SEQUENCE 359 AA; 40780 MW; 9FC46DAE798A1244 CRC64;
Query Match 15.5%; Score 254.5; DB 2; Length 359;
Best Local Similarity 23.5%; Pred. No. 1.1e-08;
Matches 72; Conservative 77; Mismatches 136; Indels 21; Gaps 11;
QY 7 PSMRGHTSRNSSC---DPIVTPHLISLYFVLIGLVGVISILFLVKNM-TRSYVTMA 62
DB 43 PNPGRGTATPNGTCPEMDKLLSLTISYVIPVGLVGNIALVYFLGIHRRKNSIQIY 102
QY 63 VINLVVHVSFLLTVPRFLTLYLIKKT-VMFGLPFCFVSAMLIHMVLTFLFYVILVTR 121
DB 103 LNVAVLADLLILPCLPRIMYHINRNQWTLGVILCKVGLFTFMNMYISIIILGFSIDR 162
QY 122 YLIFPKCKDVEFYRKL---HAAVASAGMTLVIV-IVPLVSVRGHIEYNEHC 177
DB 163 YI---KINRSIOORRAVTRKQSIYVCTVWTVLADGPSAMITTLKGNH---NSTVC 216
QY 178 HKELAYTVYK-IINMIVIFVIAVAVILLVFOVELI--MLMVQKLRHSLSHQEFMA 235

DB 217 RERHNAKGAIFVYVVLVWFVFLFLLIISYIKGNLIGISRRKSPFGSKYATARN 276
QY 236 LIFEIVIL-VCELPLYOFRILYLVNVTSHNACS SKVAFY--NEIFLSTVTAI-SCYDLLF 291
DB 277 SFVLILFVFCFPHYAFRPVYISQLNPSQVWKEIHKHNEIMLVFSSFNCLDPVMY 336
QY 292 VFGSH 297
DB 337 FLMSN 342
RESULT 10
ID Q7ZZA4 PRELIMINARY; PRT; 347 AA.
AC Q7ZZA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SI:b2462.9 (Novel protein similar to nucleotide receptors).
GN Name=pr2y41; Synonyms=SI:b2462.9, slc25a5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Shuce C.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL590151; CAD68067.1; -
DR ZFIN: ZDB-GENE-030616-77; pr2y41.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . . ; IEA.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR InterPro: IPR000018; P2Y_purinocptor.
DR InterPro: IPR002286; P2_purinocptor.
DR Pfam: PF00001; 7tm.1; 1-
DR PRINTS: PRO0237; GPCRHOOPSN.
DR PRINTS: PRO1066; P2YPRNOCPTR.
DR PRINTS: PRO1157; P2YPRNOCPTR.
DR PROSITE: PS00237; G_PROTEIN_RECBP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECBP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F83CC283E2 CRC64;
Query Match 15.3%; Score 250; DB 2; Length 347;
Best Local Similarity 24.5%; Pred. No. 2e-08;
Matches 81; Conservative 67; Mismatches 124; Indels 58; Gaps 14;
QY 9 MEGHNTSRNSSC-----DPIVTPHLISLYFVLIGLVGVISILFLVKNMTRSYVTMA 62
DB 1 MPWSSKEVNFSCFDEEFYILP--VSYLVCFGLINSVALMWFTKMPKPSIVY 58
QY 63 VINLVVHVSFLLTVPRFLTLYLIKKT-VMFGLPFCFVSAMLIHMVLTFLFYVILVTR 121
DB 59 MPTLADSLVLYLSLMLLYYANSHMPGVGLCKIVFLYANLYCSILPLTCSVNR 118
QY 122 YLIFPKCKDVEFYRKLHAAVAAAGMTLVIVVPLV---SRG---IHEEYNEH 173
DB 119 YLIGCHPISRLTLIKRHAHMYCGFMTVAVIACLVTLVNTSRGNSLTGDSRPE- 177
QY 174 EKFEKELAYTVYK-IINMIVIFVIAVAVILLVFOVELI--MLMVQKLRHSLSHQEFMA 230
DB 178 --EFHNFVTVNSV---VWVLFILFVLIYVY---CLMARALCOPRKGLAQOQSS 226
QY 231 AOLKNLFFIGVIL---CELPLYOFR-IYY-----LVNVTSHNACS SKVAFN 274
DB 227 SRKSKIKLIVLVVPAIGFVPHITRLTYAVYRIFDADCKLTINLVNFSYKILTRPLASVN 286

QY 275 EIFLSTVAISCYDLLLFVFGSHMFQKXII 304
Db 287 -----SCUDPLIYFLAGDH-YRSKLL 306

RESULT 11
ID 081V19 PRELIMINARY; PRT; 337 AA.

AC 081V19;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Cysteiny1 leukotriene receptor 1.
GN Name=CysLTR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (12)
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RU Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC035750; AAH35750.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004974; F:leukotriene receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004071; CysLeuk_receptor.
DR InterPro; IPR000276; GPCR_Knopden.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CYSLTR1.
DR PROSITE; PRO0237; GPCR_HODPSN.
DR PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 337 AA; 38485 MW; B9B09CEBFD305245 CRC64;

Query Match 15.1%; Score 247; DB 2; Length 337;
Best Local Similarity 21.9%; Pred. No. 3e-08;
Matches 68; Conservative 81; Mismatches 133; Indels 28; Gaps 11;

QY 11 GHNTSNSSC---DPIVTPHLISLYFVILIGLVVISILFLVX-MNTRSVTTMAVIN 65
Db 5 GNLTVSSATCTHDIDDFRQVSTLSTYSVGFPGFNGFLVYLITKTHKKSFAFYVMIN 64
QY 66 LVVYHVFLLTVFRFLTYLTK-TMMEGDPCEKFSVAMHIMHYLTFLLFYVILVTRYLI 124
Db 65 LAVALDLVCCTPLRVRVYVYVYHKGIMLFGDPLCRSLTYALYVNLVYCSIFPMTA-----WS 118

QY 125 PFKC-----KDXVEYRKLHVAASAGMTLVIVVPLVSRXYGHEBYNEHCPRKH 178
Db 119 FFRCAIAIPVPGNINLVYQKKARFVCGIMFVLITSSPPLMAK-PQDEKNNTCCFEP 177
QY 179 KE-LAYTVKTIINY-MIVIFVIAVAVLLVFQVFTIMAMQKRLSHLSHOEFMAQLKN 235
Db 178 QDNQTKRNVLVLYHVSFLFVGFIIPFVITIVCTMTIILTLTKSMCKNLSHKAIGMT-- 235
QY 236 LFFIGVIVVCPFPYGFPIRYILNVV-THSNCSKVAFYNEIFLSVTAIS---CYDLLLF 291
Db 236 MVTYTAFLVSEFWPIYIQRTIHFLHFNETKPCDSVLTMOKSVITLSLAISNCCFDPILY 295
QY 292 VFGSGHMFQK 301
Db 296 FPGSGNPFRR 305

RESULT 12
ID CLT1_HUMAN STANDARD; PRT; 337 AA.

AC 09Y271;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteiny1 leukotriene receptor 1 (CysLTR1) (Cysteiny1 leukotriene D4
DE receptor) (LTD4 receptor) (HG55) (HMTMF81).
GN Name=CysLTR1; Synonyms=CysLTR1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE=Tonsil;
RX MEDLINE=99318129; PubMed=10391245; DOI=10.1038/21658;
RA Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M.,
RA Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M.,
RA Bai C., Austin C.P., Chateaufneuf A., Stocco R., Greig G.M.,
RA Karman S., Hooks S.B., Hoesfeld E., Williams D.L. Jr.,
RA Ford-Hutchinson A.W., Caskey C.T., Evans J.F.,
RT "Characterization of the human cysteiny1 leukotriene CysLTR1
RT receptor";
RL Nature 399:789-793(1999).

RN (12)
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte, Peripheral blood monocytes, and Spleen;
RX MEDLINE=99393629; PubMed=10462554;
RA Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshourbagy N.,
RA Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Muddock P.R.,
RA Herlihy N.C., Halsey W., Sathe G., Muir A.I., Nuthallaganai P.,
RA Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.;
RT "Identification, molecular cloning, expression, and characterization
RT of a cysteiny1 leukotriene receptor";
RL Mol. Pharmacol. 56:657-663(1999).

RN (13)
RP SEQUENCE FROM N.A.
RA Warren C.N., Atkinson R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guttridge cDNA resource center (www.cdna.org).";
RU Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RC -!- FUNCTION: Receptor for cysteiny1 leukotrienes mediating
RC bronchoconstriction of individuals with and without asthma.
CC Stimulation by LTD4 results in the contraction and proliferation
CC of smooth muscle, edema, eosinophil migration and damage to the
CC mucus layer in the lung. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system. The rank order of affinities for the leukotrienes is LTD4
CC > LTD4 = LTC4 >> LTC4.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in
CC spleen and peripheral blood leukocytes. Lower expression in
CC several tissues, such as lung (mostly in smooth muscle bundles and
CC alveolar macrophages), placenta, small intestine, pancreas, colon

QY 172 EHCEKHEKELAYTYVK-IINMYIF--VIAVAVILVFOVFIIMVQKLRHSLSHOE 228
DB 186 NOCFHFRRRSSNGKKAENLVLVFWLVFATWVFCYVKIASLLLRVSRRERDLPNALR 245
QY 229 FMAQLKNLFFI-GVILVCFLEPYOFPFIYVL-NVVTSHNACSS--KVAFYNEIFLSTAI- 283
DB 246 YQSAKKSFFVLFLFVCFGPHAFRPPYIFVQMIHAEUCTTLOMDQTNHVVLLLSAFN 305
QY 284 SCYD-LLLFVFGGS 296
DB 306 SCLDPVMVFFLLSGS 319

Search completed: September 10, 2005, 10:08:30
Job time : 84 secs

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OM protein - protein search, using sw model

Run on: September 10, 2005, 10:00:12 ; Search time 82 seconds

(without alignments)
1954.644 Million cell updates/sec

Title: US-10-085-233b-2

Perfect score: 1637

Sequence: 1 MQKCDPSPMNGHTSRNSSC.....GSHWPKOKIIGLNCVLCR 313

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_03.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1587	96.9	305	2	Q7Z602
2	1304	79.7	305	2	Q7TOB0
3	847	51.7	247	2	Q7TQNS
4	787	48.1	152	2	Q86SP3
5	547	33.4	131	2	Q80UC5
6	532	32.5	299	2	Q8BLT7
7	277	16.9	381	2	Q6XCB1
8	262	15.0	378	2	Q6XCB2
9	254.5	15.5	359	2	Q6XCB5
10	250	15.3	347	2	Q7Z2A4
11	247	15.1	337	2	Q81V19
12	246	15.0	337	1	CLT1_HUMAN
13	246	15.0	373	2	Q6XCE7
14	245.5	15.0	339	1	CLT1_RAT
15	244.5	14.9	386	2	Q6XCB1
16	244	14.9	292	2	Q6XCB8
17	242.5	14.8	344	2	Q6XCF9
18	242.5	14.8	366	2	Q6XCG3
19	241.5	14.8	337	2	Q61YF8
20	240.5	14.7	352	1	CLT1_MOUSE
21	238	14.5	381	2	Q6XCF3
22	236	14.4	375	1	GP34_MOUSE
23	235.5	14.4	371	2	Q6XCC5
24	235	14.4	375	2	Q8BY11
25	234	14.3	322	2	Q6XCG1
26	234	14.3	354	2	Q6XGNO
27	233.5	14.3	382	2	Q6XCC2
28	233	14.2	345	1	CLT2_PIG
29	232.5	14.2	264	1	Q6XCB9
30	232	14.2	381	1	GP34_GORGO
31	232	14.2	381	1	GP34_HUMAN

32	232	14.2	381	1	GP34_PANTR	Pe0019 pan troglod
33	231.5	14.1	264	2	Q6XCF5	Q6XCF5 microtus ar
34	231.5	14.1	340	1	CLT1_PIG	Q95N02 sus scrofa
35	231.5	14.1	358	1	GP87_HUMAN	Q9B21 homo sapien
36	230.5	14.1	263	2	Q6XCF0	Q6XCF0 alces alces
37	230	14.1	312	2	Q6XCF7	Q6XCF7 canis famli
38	229.5	14.0	264	2	Q6XCF6	Q6XCF6 meriones un
39	228.5	14.0	264	2	Q6XCF1	Q6XCF1 erinaceus e
40	226.5	13.8	322	2	Q6XCF8	Q6XCF8 sus scrofa
41	226	13.8	309	1	CLT2_RAT	Q924C9 rattus norv
42	226	13.8	337	2	Q61YR5	Q924C9 rattus norv
43	225	13.7	346	1	CLT2_HUMAN	Q9N875 homo sapien
44	222	13.6	391	1	SSR1_RAT	P28646 rattus norv
45	221	13.5	391	1	SSR1_HUMAN	P30872 homo sapien

ALIGNMENTS

RESULT 1	ID	Accession	Length	Score	DB ID	Description
Q7Z602	Q7Z602	PRELIMINARY;	PRT;	305 AA.		
DT	01-OCT-2003	(TREMBlrel. 25, Created)				
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)				
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)				
DE	G protein-coupled receptor 141.					
GN	Name=GPRL141;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;					
RA	Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,					
RA	Schloth H.B.;					
RT	"seven evolutionarily conserved human rhodopsin G protein-coupled					
RT	receptors lacking close relatives."					
RL	EMBL; AY288420; AAF72129.1; -					
DR	GO; GO:0016021; C:integral to membrane; IEA.					
DR	GO; GO:0004872; F:receptor activity; IEA.					
DR	GO; GO:0001864; F:rhodopsin-like receptor activity; IEA.					
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.					
DR	PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.					
KM	Receptor.					
SO	SEQUENCE					
Query Match	96.9%;	Score 1587;	DB 2;	Length 305;		
Best Local Similarity	99.7%;	Pred. No. 3.9e-93;				
Matches	304;	Conservative	1;	Mismatches	0;	Indels
0;						
QY	9	MPHNTSRSSCDPIYTHPLISLRYVLIGLVGVISILFLVKNMTRSVTMAVNLV	68			
DB	1	MPHNTSRSSCDPIYTHPLISLRYVLIGLVGVISILFLVKNMTRSVTMAVNLV	60			
QY	69	VHSVFLTYVPRLTYLTKTMMFGLPCKEVSAMLIHHYLPFLFVVLVLTTRYLFPKC	128			
DB	61	VHSVFLTYVPRLTYLTKTMMFGLPCKEVSAMLIHHYLPFLFVVLVLTTRYLFPKC	120			
QY	129	KDVEFYRKLHVAASAGMTLVIVLVSRYGHEBYNEBHCFFKHELAYTYVKI	188			
DB	121	KDVEFYRKLHVAASAGMTLVIVLVSRYGHEBYNEBHCFFKHELAYTYVKI	180			
QY	189	INMVIYFIVAAVILVQVFTIMLMQKLAHSLSHOEFAQLKNLFFIGVILVCFP	248			
DB	181	INMVIYFIVAAVILVQVFTIMLMQKLAHSLSHOEFAQLKNLFFIGVILVCFP	240			
QY	249	YQFRIYLVNVTSHNACSSKVAFYNEIFLSTAYTSCYDILLFVFGSHPFKOKIIGLWN	308			
DB	241	YQFRIYLVNVTSHNACSSKVAFYNEIFLSTAYTSCYDILLFVFGSHPFKOKIIGLWN	300			

QY 309 CVCACR 313
DB 301 CVCACR 305

RESULT 2

Q7TOP0 PRELIMINARY; PRT; 305 AA.

DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE G protein-coupled receptor 141.

GN Name=Gpr141.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,
RA Schioth H.B.;

RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";

RL FEBS Lett. 554:381-388(2003).

DR EMBL; AY288427; AAP72136.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsn.

DR PROSITE; PS50262; G_PROTEIN_RECERP_F1_2; 1.

KM Receptor.

SQ SEQUENCE 305 AA; 35284 MW; 74C7EB210158D554 CRC64;

Query Match 79.7%; Score 1304; DB 2; Length 305;

Best Local Similarity 81.2%; Pred. No. 3 3e-75;

Matches 247; Conservative 24; Mismatches 33; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLISLYFIYVILGIVGISILFLVKNKTRSVTTMAVINLV 68

DB 1 MDEVNTSENSCDPILAHLTLFVYFIVIGIVGISILFLVKNKTRSVTTMAVINLV 60

QY 69 VHSVELLYVPEFLTYLTKTMMEGP.PCKFVSAMHIMHYLTFLLVYVILVIRYLIFFKC 128

DB 61 VHGVPFLTYVPEFLAYLTKGTWTFGLPCKFVSAMHIMHYLTFLLVYVILVIRYLIFFKC 120

QY 129 KDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 188

DB 121 RDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 180

QY 189 INMYIVFVIAVAVILVFOVFIIMLMVOKLRHSILSHOEFMAQNLNLPFGIIVLCPL 248

DB 181 INMYIVFVIAVAVILVFOVFIIMLMVOKLRHSILSHOEFMAQNLNLPFGIIVLCPL 240

QY 249 YQEFRIYLVNVTTHNAACSSKVA.FVNEIFLSTVAISCYLLLFVREGSNWFQKLTGLMN 308

DB 241 YQEFRIYLVNVTTHNAACSSKVA.FVNEIFLSTVAISCYLLLFVREGSNWFQKLTGLMN 300

QY 309 CVCAC 312

DB 301 CVCAC 304

RESULT 3

Q7TON5 PRELIMINARY; PRT; 247 AA.

DT 01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE G protein-coupled receptor 141.

GN Name=Gpr141;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,
RA Schioth H.B.;

RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";

RL FEBS Lett. 554:381-388(2003).

DR EMBL; AY288432; AAP72141.1; -.

DE G protein-coupled receptor 141.

GN Name=Gpr141;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,
RA Schioth H.B.;

RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";

RL FEBS Lett. 554:381-388(2003).

DR EMBL; AY288432; AAP72141.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsn.

DR PROSITE; PS50262; G_PROTEIN_RECERP_F1_2; 1.

KM Receptor.

SQ SEQUENCE 247 AA; 28462 MW; A677E0011BFICE51 CRC64;

Query Match 51.7%; Score 847; DB 2; Length 247;

Best Local Similarity 79.1%; Pred. No. 2 4e-46;

Matches 167; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 9 MGHNTSRNSCDPIVTPHLISLYFIYVILGIVGISILFLVKNKTRSVTTMAVINLV 68

DB 1 MDEVNTSENSCDPILAHLTLFVYFIVIGIVGISILFLVKNKTRSVTTMAVINLV 60

QY 69 VHSVELLYVPEFLTYLTKTMMEGP.PCKFVSAMHIMHYLTFLLVYVILVIRYLIFFKC 128

DB 61 VHGVPFLTYVPEFLAYLTKGTWTFGLPCKFVSAMHIMHYLTFLLVYVILVIRYLIFFKC 120

QY 129 KDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 188

DB 121 RDKVEFYRKLHAAVASAGMTLVIVIVPLVVSRYGIEHEVNEHCFFKHELAATYVKI 180

QY 189 INMYIVFVIAVAVILVFOVFIIMLMVOKLRHSILSHOEFMAQNLNLPFGIIVLCPL 248

DB 181 INMYIVFVIAVAVILVFOVFIIMLMVOKLRHSILSHOEFMAQNLNLPFGIIVLCPL 240

QY 249 YQEFRIYLVNVTTHNAACSSKVA.FVNEIFLSTVAISCYLLLFVREGSNWFQKLTGLMN 308

DB 241 YQEFRIYLVNVTTHNAACSSKVA.FVNEIFLSTVAISCYLLLFVREGSNWFQKLTGLMN 300

QY 309 CVCAC 312

DB 301 CVCAC 304

RESULT 4

Q86SP3 PRELIMINARY; PRT; 152 AA.

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE G protein-coupled receptor GPR13 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergmann J.E., Galanakis G.A.;

RT "The G protein-coupled receptor repertoire of human and mouse.";

RT Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).

RL EMBL; AY255538; AA085050.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsn.

DR PROSITE; PS50262; G_PROTEIN_RECERP_F1_2; 1.

KM Receptor.

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OM protein - protein search, using sw model

Run on: September 10, 2005, 03:07:41 ; Search time 27 Seconds
(without alignments)
865.376 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637

Sequence: 1 MOKDPPSPMGHTSHNSC.....GSHWFQKILGLMNCVLCR 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents_AA:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	229	14.6	337	3	US-09-044-404A-2
2	232	14.6	337	4	US-09-586-924-2
3	232	14.2	381	4	US-09-745-842-21
4	231	14.1	358	4	US-08-988-876-3
5	231	14.1	358	4	US-09-919-172-22
6	223	13.6	346	4	US-09-585-876-2
7	221	13.5	391	1	US-07-816-283-2
8	221	13.5	391	1	US-07-816-283-2
9	221	13.5	391	1	US-08-417-103-4
10	221	13.5	391	1	US-08-417-103-4
11	221	13.5	391	1	US-08-417-103-4
12	221	13.5	391	1	US-08-417-103-4
13	219	13.4	344	2	US-08-467-948A-8
14	219	13.4	344	2	US-08-467-948A-8
15	217.5	13.3	355	4	US-08-833-752-9
16	217.5	13.3	355	4	US-09-938-719-9
17	217.5	13.3	355	4	US-09-938-719-9
18	216	13.2	391	3	US-09-939-226B-9
19	215	13.1	331	4	US-09-170-496D-36
20	214	13.1	325	2	US-08-467-948A-29
21	214	13.1	325	2	US-08-467-948A-29
22	214	13.1	328	1	US-08-148-215A-2
23	214	13.1	328	4	US-09-170-496D-12
24	214	13.1	328	4	US-09-170-496D-12
25	214	13.1	338	3	US-08-988-876-8
26	214	13.1	338	3	US-09-303-524A-2
27	214	13.1	338	4	US-09-745-842-13

28	214	13.1	338	4	US-09-919-497-77	Sequence 77, Appl
29	214	13.1	339	4	US-09-170-496D-182	Sequence 182, App
30	213	13.0	331	4	US-09-910-695-4	Sequence 4, Appl1
31	212.5	13.0	389	3	US-08-430-286A-7	Sequence 7, Appl1
32	211	12.9	369	4	US-09-826-509-571	Sequence 571, App
33	208.5	12.7	381	1	US-08-467-125-2	Sequence 2, Appl1
34	208.5	12.7	381	2	US-08-911-320A-2	Sequence 2, Appl1
35	208.5	12.7	381	3	US-09-217-101-2	Sequence 2, Appl1
36	208	12.7	331	4	US-09-170-496D-184	Sequence 184, App
37	208	12.7	335	4	US-09-170-496D-2	Sequence 2, Appl1
38	207.5	12.7	355	1	US-08-012-988A-2	Sequence 2, Appl1
39	207.5	12.7	355	1	US-08-450-393A-5	Sequence 5, Appl1
40	207.5	12.7	355	3	US-08-446-669-5	Sequence 5, Appl1
41	207.5	12.7	355	3	US-09-239-938-1	Sequence 1, Appl1
42	207.5	12.7	355	4	US-09-886-319A-14	Sequence 14, Appl1
43	207.5	12.7	355	4	US-10-039-659A-13	Sequence 13, Appl1
44	207.5	12.7	355	4	US-09-561-068-1	Sequence 1, Appl1
45	207.5	12.7	355	4	US-09-625-573-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1

US-09-044-404A-2

Sequence 2, Application US/09044404A

Patent No. 6200775

GENERAL INFORMATION:

APPLICANT: SATHI, GANESH

APPLICANT: HALSEY, WENDY

APPLICANT: ELIS, CATHERINE

APPLICANT: AMES, ROBERT

APPLICANT: FOLEY, JAMES

APPLICANT: SARAU, HENRY

TITLE OF INVENTION: CDNA CLONE HMTF81 THAT ENCODES

TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: SmithKline Beecham Corporation

STREET: 790 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,404A

FILING DATE: MARCH 19, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/844,795

FILING DATE: APRIL 22, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T.

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: GH-70001-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-044-404A-2


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/ Patent No. 6063596
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Bandman, Olga
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Yue, Henry
/ TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
/ TITLE OF INVENTION: WITH IMMUNE RESPONSE
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/988,876
/ FILING DATE: Herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0441 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: PROSTUT09
/ CLONE: 1650519
/ US-08-988-876-3

Query Match          14.1%; Score 231; DB 3; Length 358;
Best Local Similarity 24.3%; Pred. No. 4,4e-13;
Matches 76; Conservative 59; Mismatches 144; Indels 34; Gaps 10;

QY 10 PGHNTSRNSCDPIYTPHLISLYFI--VLIGLVGYSILFLVKNKNTSVTTMAVINLV 67
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Db 30 PCKNTTLHNEFDPIVLPVLYLIIFVASILLNGIA-----VWIFPHIRNKTSPFIYKNIIV 84
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 68 VVHSVFLTVPPRLTYLIK-KTMMEGLPCKFVSAMLHIMTLFIFYVIVLITRLIF 126
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 VADLMTLTFPPRIYHDAFGFPMYEFKILCRYTSVLFFVNMVTSIVFGLISIDRYLKIV 144
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 127 KCKDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGIIHEEYNEBHCFFKHELAITYV 186
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 KFGGDSRMVSIPTFKVLSVCWAVIMAVLSLPMIILNQPTEDNHDCSKLSPGKVN 204
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 187 KIINMIVIFVAVAVILVFOVFITMLMVOKLRHSLSHQEFMAQLK-----LFF 238
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 205 TAVTYVNSCLFVAIVVILIGCYIAI-----SRVYHKSSROFISQSSRKRNOSIRV 257
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 229 IGVILVCLPYQFPRI-----YLVNVTSHNACSSKVAFY-NEIFLSVTAIS-CYDLLLFV 292
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 258 VAVYTCFPLPYHLCRMPSTFSLHDLRLDESA--QKILVYCKEITFLSACNVCLDPIIYF 315
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 293 F---GGSWFKOK 302
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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Db 316 FMCRSFSRWLFKK 328

RESULT 5
US-09-919-172-22
/ Sequence 22, Application US/09919172
/ Patent No. 6673545
/ GENERAL INFORMATION:
/ APPLICANT: Paris, Mary
/ APPLICANT: Turner, Christopher M.
/ TITLE OF INVENTION: PROSTATE CANCER MARKERS
/ FILE REFERENCE: PA-0036 US
/ CURRENT APPLICATION NUMBER: US/09/919,172
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/222,469
/ PRIOR FILING DATE: 2000-07-28
/ SOFTWARE: PERL Program
/ SEQ ID NO 22
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6673545 1650519CD1
US-09-919-172-22

Query Match          14.1%; Score 231; DB 4; Length 358;
Best Local Similarity 24.3%; Pred. No. 4,4e-13;
Matches 76; Conservative 59; Mismatches 144; Indels 34; Gaps 10;

QY 10 PGHNTSRNSCDPIYTPHLISLYFI--VLIGLVGYSILFLVKNKNTSVTTMAVINLV 67
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 30 PCKNTTLHNEFDPIVLPVLYLIIFVASILLNGIA-----VWIFPHIRNKTSPFIYKNIIV 84
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 68 VVHSVFLTVPPRLTYLIK-KTMMEGLPCKFVSAMLHIMTLFIFYVIVLITRLIF 126
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 VADLMTLTFPPRIYHDAFGFPMYEFKILCRYTSVLFFVNMVTSIVFGLISIDRYLKIV 144
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 127 KCKDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGIIHEEYNEBHCFFKHELAITYV 186
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 KFGGDSRMVSIPTFKVLSVCWAVIMAVLSLPMIILNQPTEDNHDCSKLSPGKVN 204
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 187 KIINMIVIFVAVAVILVFOVFITMLMVOKLRHSLSHQEFMAQLK-----LFF 238
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 205 TAVTYVNSCLFVAIVVILIGCYIAI-----SRVYHKSSROFISQSSRKRNOSIRV 257
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 229 IGVILVCLPYQFPRI-----YLVNVTSHNACSSKVAFY-NEIFLSVTAIS-CYDLLLFV 292
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 258 VAVYTCFPLPYHLCRMPSTFSLHDLRLDESA--QKILVYCKEITFLSACNVCLDPIIYF 315
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 293 F---GGSWFKOK 302
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 316 FMCRSFSRWLFKK 328
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
US-09-585-876-2
/ Sequence 2, Application US/09585876
/ Patent No. 6586205
/ GENERAL INFORMATION:
/ APPLICANT: Glucksmann, Maria Alexandra
/ APPLICANT: Slios-Santiago, Immaculada
/ TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like molecule and
/ TITLE OF INVENTION: Uses Thereof
/ FILE REFERENCE: 5800-88
/ CURRENT APPLICATION NUMBER: US/09/585,876
/ CURRENT FILING DATE: 2000-06-01
/ EARLIER APPLICATION NUMBER: 60/182,061
/ EARLIER FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
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Db 271 LMVAVVVFVLCMP--FYVQLVNFVFEQDDATVSQLSVILGYSANCPILYGLSD 328
QY 273 -YNEIFLVSATASCYD 287
Db 329 NFKRSFORILCLSMWD 344

RESULT 13

US-08-467-948A-8
Sequence 8, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-948A-8

Query Match 13.4%; Score 219; DB 2; Length 344;

Best Local Similarity 27.1%; Pred. No. 5e-12;
Matches 75; Conservative 54; Mismatches 128; Indels 20; Gaps 12;

QY 31 LKFTVLIGLV-GVISILFLVKNTRSVTMAVINLVVHVSFLLTVPRRLTYLIKKTW 89
Db 23 MFSWVFLGLISNCVAIYIFICVLKVRNETTYMINLMSDILFVFTLPFRIFPTTRW 82
QY 90 MFGLPCKFVSAMLIHMYLTFLLFYVVLILVTRYL-IFPKCKDKVEFYRKLHVAASAGW 148
Db 83 PFGDLCKISVMLFYTMGSIILFTLCISVDRFLAIYVPPSKT-LRTKRNKIVCTGVM 141
QY 149 TLVIIVVPLVVSRYGHEBYN--BEHCFFKELAY-TYVKIINMYIVFIAVAVIL- 204
Db 142 LTVIGSAPAVFVQ-STHSGNNASEACFENFPEATWTKYLS---RIVIFIEIVGFIP 196
QY 205 LVQGVFIMLMVQKLRLSL-LSHOEF-MAQLKNLFFIGVIL--VCPLPYGFPRIYIYNV 260

Db 197 LILNVTCSSMVLKTLKRPVTLSSRKINKKVLKMIFFVHLIIFPCFCVPININILXSVR 256
QY 261 THSNACSSKVAFYNEIFLVSATAS---CYDLLFVF 293
Db 257 TQTFVNCVVAAVRTMYPITLCIAVNCFCFDPVYVF 293

RESULT 14

US-08-467-947A-8
Sequence 8, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-947A-8

Query Match 13.4%; Score 219; DB 3; Length 344;

Best Local Similarity 27.1%; Pred. No. 5e-12;
Matches 75; Conservative 54; Mismatches 128; Indels 20; Gaps 12;

QY 31 LKFTVLIGLV-GVISILFLVKNTRSVTMAVINLVVHVSFLLTVPRRLTYLIKKTW 89
Db 23 MFSWVFLGLISNCVAIYIFICVLKVRNETTYMINLMSDILFVFTLPFRIFPTTRW 82
QY 90 MFGLPCKFVSAMLIHMYLTFLLFYVVLILVTRYL-IFPKCKDKVEFYRKLHVAASAGW 148
Db 83 PFGDLCKISVMLFYTMGSIILFTLCISVDRFLAIYVPPSKT-LRTKRNKIVCTGVM 141
QY 149 TLVIIVVPLVVSRYGHEBYN--BEHCFFKELAY-TYVKIINMYIVFIAVAVIL- 204
Db 142 LTVIGSAPAVFVQ-STHSGNNASEACFENFPEATWTKYLS-----RIVIFIEIVGFIP 196

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2005, 07:21:37 ; Search time 75 Seconds

(without alignments)
1646.094 Million cell updates/sec

Title: US-10-085-233B-2

Perfect score: 1637

Sequence: 1 MQKDFPSMGHTSRNSSC.....GGSHPKQKIGLVNCLCR 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1634	99.8	313	16	US-10-467-252-4
3	1610	98.4	312	10	US-09-782-974C-82
4	1610	98.4	312	17	US-10-467-492A-82
5	1610	98.4	312	17	US-10-975-979-82
6	1610	98.4	367	16	US-10-467-252-6
7	1610	98.4	448	15	US-10-292-798-1008
8	1587	96.9	305	9	US-09-995-225-4
9	1587	96.9	305	10	US-09-995-225-4
10	1587	96.9	305	14	US-10-055-106C-2
11	1567	96.9	305	14	US-10-188-405-10

12	1587	96.9	305	14	US-10-293-171-2	Sequence 2, Appl1
13	1587	96.9	305	14	US-10-017-161-1194	Sequence 1194, Ap
14	1587	96.9	305	14	US-10-366-504-7	Sequence 7, Appl1
15	1587	96.9	305	15	US-10-297-908A-1	Sequence 1, Appl1
16	1587	96.9	305	16	US-10-467-252-5	Sequence 5, Appl1
17	1587	96.9	543	17	US-10-505-486-110	Sequence 110, App
18	1526	93.2	339	16	US-10-398-036-6	Sequence 6, Appl1
19	1141	69.7	269	14	US-10-366-504-2	Sequence 2, Appl1
20	548	33.5	149	10	US-09-782-974C-22	Sequence 22, Appl1
21	548	33.5	149	17	US-10-467-492A-22	Sequence 22, Appl1
22	548	33.5	149	17	US-10-975-979-22	Sequence 22, Appl1
23	249	15.2	337	14	US-10-290-078-21	Sequence 21, Appl1
24	247	15.1	337	14	US-10-167-192-3	Sequence 3, Appl1
25	247	15.1	337	15	US-10-400-991-6	Sequence 6, Appl1
26	246	15.0	337	9	US-09-866-230-8	Sequence 8, Appl1
27	246	15.0	337	9	US-09-828-478-5	Sequence 5, Appl1
28	246	15.0	337	10	US-09-991-225-6	Sequence 6, Appl1
29	246	15.0	337	14	US-10-055-106C-3	Sequence 3, Appl1
30	246	15.0	337	14	US-10-225-567A-547	Sequence 547, App
31	246	15.0	337	14	US-10-349-021-5	Sequence 5, Appl1
32	246	15.0	337	15	US-10-369-405-6	Sequence 6, Appl1
33	246	15.0	337	15	US-10-692-605-4	Sequence 4, Appl1
34	246	15.0	337	18	US-10-499-172-19	Sequence 19, Appl1
35	239	14.6	337	10	US-09-779-679-27	Sequence 27, Appl1
36	236	14.4	375	18	US-10-499-172-22	Sequence 22, Appl1
37	233	14.2	345	17	US-10-932-004-18	Sequence 18, Appl1
38	232	14.2	381	10	US-09-745-842-21	Sequence 21, Appl1
39	232	14.2	381	14	US-10-225-567A-414	Sequence 414, App
40	232	14.2	381	16	US-10-473-127-1417	Sequence 1417, Ap
41	232	14.2	381	16	US-10-473-127-1418	Sequence 1418, Ap
42	232	14.2	381	16	US-10-473-127-1420	Sequence 1420, Ap
43	232	14.2	381	16	US-10-473-127-1421	Sequence 1421, Ap
44	232	14.2	381	16	US-10-473-127-1423	Sequence 1423, Ap
45	232	14.2	381	16	US-10-473-127-1425	Sequence 1425, Ap

ALIGNMENTS

RESULT 1									
US-10-085-233B-2									
; Sequence 2, Application US/10085233B									
; Publication No. US20030087249A1									
; GENERAL INFORMATION:									
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA									
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED									
; FILE REFERENCE: RECEPTOR AND USES THEREFOR									
; CURRENT APPLICATION NUMBER: US/10/085,233B									
; CURRENT FILING DATE: 2002-02-28									
; PRIOR APPLICATION NUMBER: 60/272,677									
; PRIOR FILING DATE: 2001-03-01									
; NUMBER OF SEQ ID NOS: 6									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 313									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-085-233B-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 1.4e-134;									
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MQKDFPSMGHTSRNSSC	PIVPHILSLFYILGSLVGVISILFLVVMNTRSVTT	60					
DB	1	MQKDFPSMGHTSRNSSC	PIVPHILSLFYILGSLVGVISILFLVVMNTRSVTT	60					
QY	61	MAVINLVVHVSFLLTVPRLLTYLLIKTWMFGLPCKEVSAMLIHMYLTFLLFYVILVT	120						
DB	61	MAVINLVVHVSFLLTVPRLLTYLLIKTWMFGLPCKEVSAMLIHMYLTFLLFYVILVT	120						
QY	121	RYLIFFKCKDKVEFPRKRLHANAASAGMTLVIVVPLVVSRYGIEHYEENBHCFFHKE	180						

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|||||
Db 121 RYLIFPKCKDKVEFYRKLHAVAASAGMMTLVIVVPLVVSRYGHEEYNEHCXFKHKE 180
QY 181 LATVYKLIINMIVIVIAVAIVLLVFOVFIIMLVOKLRSHLSHOEFMAQLKNLFFLG 240
Db 181 LATVYKLIINMIVIVIAVAIVLLVFOVFIIMLVOKLRSHLSHOEFMAQLKNLFFLG 240
QY 241 VILVCFLEPYQFPRRIYYLINVVTHSNACSSKVAFYNEIFLSTVAISCYDLLLFFVGGSHMFK 300
Db 241 VILVCFLEPYQFPRRIYYLINVVTHSNACSSKVAFYNEIFLSTVAISCYDLLLFFVGGSHMFK 300
QY 301 QKIIGLMNCVLCR 313
Db 301 QKIIGLMNCVLCR 313

RESULT 2
US-10-467-252-4
; Sequence 4, Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.
; APPLICANT: ARVIZU, Chandra S.; ELIOTT, Vicki S.;
; APPLICANT: HAFILIA, April J.A.; RAMKOMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y.Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dyang Aina M.;
; APPLICANT: GRAUB, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Rodrick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFPIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junming;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10467,252
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 90012430CD1
US-10-467-252-4

Query Match 99.8%; Score 1634; DB 16; Length 313;
Best Local Similarity 99.7%; Pred. No. 2,5e-134;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKCDPSPMGHNTSRNSSCDPIVTPHILSLYFIVLIGLVGIVISILFLVKNKTRTSVTT 60
Db 1 MOKCDPSPMGHNTSRNSSCDPIVTPHILSLYFIVLIGLVGIVISILFLVKNKTRTSVTT 60
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QY 61 MAVINLVVHVSFLLTVPEPRLTYLLIKTWMFGLPCKEVSAMLIHMYLTFLFYVILVT 120
Db 61 MAVINLVVHVSFLLTVPEPRLTYLLIKTWMFGLPCKEVSAMLIHMYLTFLFYVILVT 120
QY 121 RYLIFPKCKDKVEFYRKLHAVAASAGMMTLVIVVPLVVSRYGHEEYNEHCXFKHKE 180
Db 121 RYLIFPKCKDKVEFYRKLHAVAASAGMMTLVIVVPLVVSRYGHEEYNEHCXFKHKE 180
QY 181 LATVYKLIINMIVIVIAVAIVLLVFOVFIIMLVOKLRSHLSHOEFMAQLKNLFFLG 240
Db 181 LATVYKLIINMIVIVIAVAIVLLVFOVFIIMLVOKLRSHLSHOEFMAQLKNLFFLG 240
QY 241 VILVCFLEPYQFPRRIYYLINVVTHSNACSSKVAFYNEIFLSTVAISCYDLLLFFVGGSHMFK 300
Db 241 VILVCFLEPYQFPRRIYYLINVVTHSNACSSKVAFYNEIFLSTVAISCYDLLLFFVGGSHMFK 300
QY 301 QKIIGLMNCVLCR 313
Db 301 QKIIGLMNCVLCR 313

RESULT 3
US-09-782-974C-82
; Sequence 82, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogelii, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-82

Query Match 98.4%; Score 1610; DB 10; Length 312;
Best Local Similarity 99.7%; Pred. No. 3.1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPPSPMGHNTSRNSSCDPIVTPHILSLYFIVLIGLVGIVISILFLVKNKTRTSVTTMAVI 64
Db 4 DPPSPMGHNTSRNSSCDPIVTPHILSLYFIVLIGLVGIVISILFLVKNKTRTSVTTMAVI 63
QY 65 NLVVHVSFLLTVPEPRLTYLLIKTWMFGLPCKEVSAMLIHMYLTFLFYVILVTRYL 124
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DB 64 NLVVHVSFLITVPRFLTYLTKTWMGGLPFCKFVSAMLHMYLTFLLFVVLVTRYYL 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 303
QY 305 GLMNCVLCR 313
DB 304 GLMNCVLCR 312
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RESULT 4

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US-10-467-492A-82
; Sequence 82, Application US/10467492A
; Publication No. US2005069976A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: Novel G Protein Coupled Receptor
; FILE REFERENCE: 0411PHRM313
; CURRENT APPLICATION NUMBER: US/10/467,492A
; CURRENT FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-492A-82
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Query Match 98.4%; Score 1610; DB 17; Length 312;
Best Local Similarity 99.7%; Pred. No. 3,1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 5 DFPSPMGHNTSRNSCDPIVTPHLSLTYFIVLIGLVGVSILFLVKNNTSRVTMMAYI 64
DB 4 DFPSPMGHNTSRNSCDPIVTPHLSLTYFIVLIGLVGVSILFLVKNNTSRVTMMAYI 63
QY 65 NLVVHVSFLITVPRFLTYLTKTWMGGLPFCKFVSAMLHMYLTFLLFVVLVTRYYL 124
DB 64 NLVVHVSFLITVPRFLTYLTKTWMGGLPFCKFVSAMLHMYLTFLLFVVLVTRYYL 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 303
QY 305 GLMNCVLCR 313
DB 304 GLMNCVLCR 312
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RESULT 5
US-10-975-979-82

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; Sequence 82, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Scheinin, Kathleen
; APPLICANT: Bannigan, Chris
; APPLICANT: Huff, Valerie
; APPLICANT: Kayes, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Parodi, Luis
; APPLICANT: Hiesch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PHRM293
; CURRENT APPLICATION NUMBER: US/10/975,979
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-979-82
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Query Match 98.4%; Score 1610; DB 17; Length 312;
Best Local Similarity 99.7%; Pred. No. 3,1e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 5 DFPSPMGHNTSRNSCDPIVTPHLSLTYFIVLIGLVGVSILFLVKNNTSRVTMMAYI 64
DB 4 DFPSPMGHNTSRNSCDPIVTPHLSLTYFIVLIGLVGVSILFLVKNNTSRVTMMAYI 63
QY 65 NLVVHVSFLITVPRFLTYLTKTWMGGLPFCKFVSAMLHMYLTFLLFVVLVTRYYL 124
DB 64 NLVVHVSFLITVPRFLTYLTKTWMGGLPFCKFVSAMLHMYLTFLLFVVLVTRYYL 123
QY 125 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 184
DB 124 FPKCKDKVEFRYKLAHVAASAGMNTLVIVVPLVSRYGHEEYNEHCFFKHELAYT 183
QY 185 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 244
DB 184 YVKIINMIVIFVIAVAVILLVFOVFIIMLVOKLRHSLSHOEFMAQLKNLFFIGVILV 243
QY 245 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 304
DB 244 CFLPYQFFRIYYLNVVTHSNACSKVAFYNEIFLSVTAISCYDLLLFFVGGSHWFKOKII 303
QY 305 GLMNCVLCR 313
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Db 304 GLMNCVLCR 312

RESULT 6
US-10-467-252-6

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/ Sequence 6, Application US/10467252
/ Publication No. US20040115676A1
/ GENERAL INFORMATION:
/ APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
/ APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
/ APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
/ APPLICANT: GANDHI, Ameena R.; CHAWLA, Nandinder K.
/ APPLICANT: ARVIZU, Chandra S.; ELIOTT, Yicki S.;
/ APPLICANT: HAFALIA, April J.A.; RAMKUMAR, Jayalaxmi;
/ APPLICANT: JIN, Pei; TANG, Y.Tom;
/ APPLICANT: YUE, Henry; REDDY, Roopa
/ APPLICANT: BURFORD, Neil; LU, Dyrng Aina M.;
/ APPLICANT: GRAU, Richard C.; KAHN, Farrah A.;
/ APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
/ APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
/ APPLICANT: WARREN, Bridget A.; YANG, Junling;
/ APPLICANT: LEE, Ernestine A.; HARLAND, Lee
/ TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
/ FILE REFERENCE: PI-0357 USN
/ CURRENT APPLICATION NUMBER: US/10/467,252
/ PRIOR FILING DATE: 2003-08-06
/ PRIOR APPLICATION NUMBER: PCT/US02/03635
/ PRIOR FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: US 60/267,322;
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: US 60/271,215
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: US 60/274,551
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 60/278,507
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 60/280,597
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: US 60/281,107
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/282,121
/ PRIOR FILING DATE: 2001-04-06
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: PERL Program
/ SEQ ID NO 6
/ LENGTH: 367
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 90012670CD1
US-10-467-252-6
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Query Match 98.4%; Score 1610; DB 16; Length 367;
Best Local Similarity 99.7%; Pred. No. 3.7e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 5 DDPSPMGHTSRNSSCDPIVTPHLISLYFYVILIGLVGVISILFLVNMNTRSVTTMAVI 64
Db 59 DDPSPMGHTSRNSSCDPIVTPHLISLYFYVILIGLVGVISILFLVNMNTRSVTTMAVI 118
QY 65 NLVVHSAVFLTVPPRLTYLLIKTTMFGLPCKEVSAMLHMVLTFLFYVILVTRXYLI 124
Db 119 NLVVHSAVFLTVPPRLTYLLIKTTMFGLPCKEVSAMLHMVLTFLFYVILVTRXYLI 178
QY 125 PFCKCKDVEFYRKLAHVAASAGMNTLVIVPLVVSRYGHEEYNEEHCFKHKLAYT 184
Db 179 PFCKCKDVEFYRKLAHVAASAGMNTLVIVPLVVSRYGHEEYNEEHCFKHKLAYT 238
QY 185 YKTIINMIVIFVIAVAAILLVFQVFIIMLVQKLRHSLLSHOFWMAQLKNLFFIGVILV 244
Db 239 YKTIINMIVIFVIAVAAILLVFQVFIIMLVQKLRHSLLSHOFWMAQLKNLFFIGVILV 298
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QY 245 CELPYQFRIYYLANVVTSHNACSSKVAFYNEIFLSVTAISCYDLLFFYGGSHWFKOKII 304
Db 299 CELPYQFRIYYLANVVTSHNACSSKVAFYNEIFLSVTAISCYDLLFFYGGSHWFKOKII 358
QY 305 GLMNCVLCR 313
Db 359 GLMNCVLCR 367
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RESULT 7
US-10-292-798-1008

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/ Sequence 1008, Application US/10292798
/ Publication No. US20030235833A1
/ GENERAL INFORMATION:
/ APPLICANT: SUMA, MAKIRO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
/ FILE REFERENCE: 084335/166
/ CURRENT APPLICATION NUMBER: US/10/292,798
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: 10/017,161
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: JP 2001-246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2070
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1008
/ LENGTH: 448
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-292-798-1008
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Query Match 98.4%; Score 1610; DB 15; Length 448;
Best Local Similarity 99.7%; Pred. No. 4.6e-132;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 5 DDPSPMGHTSRNSSCDPIVTPHLISLYFYVILIGLVGVISILFLVNMNTRSVTTMAVI 64
Db 4 DDPSPMGHTSRNSSCDPIVTPHLISLYFYVILIGLVGVISILFLVNMNTRSVTTMAVI 63
QY 65 NLVVHSAVFLTVPPRLTYLLIKTTMFGLPCKEVSAMLHMVLTFLFYVILVTRXYLI 124
Db 64 NLVVHSAVFLTVPPRLTYLLIKTTMFGLPCKEVSAMLHMVLTFLFYVILVTRXYLI 123
QY 125 PFCKCKDVEFYRKLAHVAASAGMNTLVIVPLVVSRYGHEEYNEEHCFKHKLAYT 184
Db 124 PFCKCKDVEFYRKLAHVAASAGMNTLVIVPLVVSRYGHEEYNEEHCFKHKLAYT 183
QY 185 YKTIINMIVIFVIAVAAILLVFQVFIIMLVQKLRHSLLSHOFWMAQLKNLFFIGVILV 244
Db 184 YKTIINMIVIFVIAVAAILLVFQVFIIMLVQKLRHSLLSHOFWMAQLKNLFFIGVILV 243
QY 245 CELPYQFRIYYLANVVTSHNACSSKVAFYNEIFLSVTAISCYDLLFFYGGSHWFKOKII 304
Db 244 CELPYQFRIYYLANVVTSHNACSSKVAFYNEIFLSVTAISCYDLLFFYGGSHWFKOKII 303
QY 305 GLMNCVLCR 313
Db 304 GLMNCVLCR 312
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RESULT 8
US-09-995-225-4

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/ Sequence 4, Application US/09995225
/ Publication No. US20020193584A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Chu, Zhi Liang
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Lowitz, Kevin P.
```

```
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human C
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-225-4
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Query Match          96.9%; Score 1587; DB 9; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 9 MPGHNTSRNSSCDPIVTPHLSLYFIYVLIGLVGISILFLVKNMTRSVTTMAVINLV 68
DB 1 MPGHNTSRNSSCDPIVTPHLSLYFIYVLIGLVGISILFLVKNMTRSVTTMAVINLV 60
QY 69 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 128
DB 61 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 120
QY 129 KDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHELAITYYVKI 188
DB 121 KDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHELAITYYVKI 180
QY 189 INMYIVFVIAVAVILVFOVEFIIMLMVQKLHSHLSHOFMAQKNLFFIGVILVCFPL 248
DB 181 INMYIVFVIAVAVILVFOVEFIIMLMVQKLHSHLSHOFMAQKNLFFIGVILVCFPL 240
QY 249 YQFFRIYYLNVVTHSNACSKVAFYNEIFLSTVAISCYDILLFVFGSGHWFKOKIIGLWN 308
DB 241 YQFFRIYYLNVVTHSNACSKVAFYNEIFLSTVAISCYDILLFVFGSGHWFKOKIIGLWN 300
QY 309 CVLCR 313
DB 301 CVLCR 305
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RESULT 9
US-09-995-225-4
; Sequence 4, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
```

```
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Hong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-225-4
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Query Match          96.9%; Score 1587; DB 10; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 69 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 128
DB 61 VHSVFLITVPFRLTYLIKTTMFGLPCKFVSAMLHIHMYLTFLFYVVLVTRYYLIFPKC 120
QY 129 KDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHELAITYYVKI 188
DB 121 KDKVEFYRKLAAVAASAGMTLVIVVPLVVSRYGHEEYNEHCFFKHELAITYYVKI 180
QY 189 INMYIVFVIAVAVILVFOVEFIIMLMVQKLHSHLSHOFMAQKNLFFIGVILVCFPL 248
DB 181 INMYIVFVIAVAVILVFOVEFIIMLMVQKLHSHLSHOFMAQKNLFFIGVILVCFPL 240
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RESULT 10
US-10-055-106C-2
; Sequence 2, Application US/10055106C
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/ Publication No. US20030017536A1
/ GENERAL INFORMATION:
/ APPLICANT: Pfizer Inc.
/ APPLICANT: Harland, Lee
/ TITLE OF INVENTION: Novel Polypeptide
/ FILE REFERENCE: PC10970AGLK
/ CURRENT APPLICATION NUMBER: US/10/055,106C
/ CURRENT FILING DATE: 2002-01-23
/ PRIOR APPLICATION NUMBER: GB0101739.1
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: US 60/267,341
/ PRIOR FILING DATE: 2001-02-08
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-055-106C-2
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Query Match          96.9%; Score 1587; DB 14; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGHNTSRNSCDPIVTPHLISLYPIVLIGLVGISILFLVKNMTRSVTTMAVINLV 60
QY VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 128
DB 61 VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 180
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DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHQEFMAQKLNLFPGVILVCFLP 240
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QY 309 CYLCR 313
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RESULT 11
US-10-188-405-10
/ Sequence 10, Application US/10188405
/ Publication No. US20030082585A1
/ GENERAL INFORMATION:
/ APPLICANT: Tian, Hui
/ APPLICANT: Dai, Kang
/ APPLICANT: Chen, Jin-long
/ APPLICANT: Zhao, Jiagang
/ APPLICANT: Cui, Gene
/ APPLICANT: Tularik Inc.
/ TITLE OF INVENTION: No. US20030082585A1e1 Receptors
/ FILE REFERENCE: 018781-008410US
/ CURRENT APPLICATION NUMBER: US/10/188,405
/ CURRENT FILING DATE: 2002-07-01
/ PRIOR APPLICATION NUMBER: US 60/302,800
/ PRIOR FILING DATE: 2001-07-03
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
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/ OTHER INFORMATION: human TGR343
US-10-188-405-10
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Query Match          96.9%; Score 1587; DB 14; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGHNTSRNSCDPIVTPHLISLYPIVLIGLVGISILFLVKNMTRSVTTMAVINLV 60
QY VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 128
DB 61 VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 180
QY 189 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHQEFMAQKLNLFPGVILVCFLP 248
DB 181 INYMIIVFVIAVAVILLVFOVFIIMLMVQKLRHSLSHQEFMAQKLNLFPGVILVCFLP 240
QY 249 YQFFRIYYLANVYTHSNACSSKVAFYNEIFLSTVTAISCYDLLFPVGGSHWFKOKIIGLMN 308
DB 241 YQFFRIYYLANVYTHSNACSSKVAFYNEIFLSTVTAISCYDLLFPVGGSHWFKOKIIGLMN 300
QY 309 CYLCR 313
DB 301 CYLCR 305
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RESULT 12
US-10-293-171-2
/ Sequence 2, Application US/10293171
/ Publication No. US20030138418A1
/ GENERAL INFORMATION:
/ APPLICANT: Bishngdrelo, Haifeng
/ APPLICANT: Cai, Jidong
/ APPLICANT: Gassenhuber, Johann
/ TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH
/ FILE REFERENCE: USAV2001/0158 US NP
/ CURRENT APPLICATION NUMBER: 2002-11-13
/ CURRENT FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: US60/354,150
/ PRIOR FILING DATE: 2001-11-13
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-293-171-2
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Query Match          96.9%; Score 1587; DB 14; Length 305;
Best Local Similarity 99.7%; Pred. No. 3.1e-130;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGHNTSRNSCDPIVTPHLISLYPIVLIGLVGISILFLVKNMTRSVTTMAVINLV 60
QY VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 128
DB 61 VHSVFLLVTPPRLTYLIKKTMMFGLPCKFVSAMLIHMVLTPLFYVILVTRYLIFPKC 120
QY 129 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 188
DB 121 KDKVEFYRKLHAVAASAGMTLVIVVPLVSVRGHIEEYNEBHCFFKHELAATYVKI 180
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Best Local Similarity	99.7%;	Pred. No. 3.1e-130;		
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Db	121	KDKVEFYRKLHVAASAGMTLVIIVVBLVVSRYGHEEYNEBEHCFKHELAITYYKI	180
Qy	189	INMYIVIFVIAVAVILVQVFIIMLMVOKLRHSLSHOEFMAOLKNLFFIGVILVCFLP	248
Db	181	INMYIVIFVIAVAVILVQVFIIMLMVOKLRHSLSHOEFMAOLKNLFFIGVILVCFLP	240
Qy	249	YQFFRIYYLNVVTHSNACSSKVAFNIEIFLSVTAISCYDLLFVFGGSHWFKOKIIGLMN	308
Db	241	YQFFRIYYLNVVTHSNACNSKVAFNIEIFLSVTAISCYDLLFVFGGSHWFKOKIIGLMN	300
Qy	309	CVLGR 313	
Db	301	CVLGR 305	

Search completed: September 10, 2005, 10:05:35
 Job time : 76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:50:20 ; Search time 4221.38 Seconds
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Title: US-10-085-233B-3

Perfect score: 939
Sequence: 1 atgcacaaatgctacttccc.....ggaaatcgtgttctgtgcgcgt 939

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	928.2	98.8	1340	6	AX709194 Sequence
3	928.2	98.8	1460	6	AX709195 Sequence
4	928.2	98.8	2525	6	AX147836 Sequence
5	928.2	98.8	2525	6	AX521885 Sequence
6	927.8	98.8	113306	6	AX646815 Sequence
7	927.8	98.8	218186	6	AC083865 Sequence
8	927.8	98.8	1332	6	CQ737895 Sequence
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11	913.4	97.3	918	6	BD187510 Novel Pol
12	913.4	97.3	918	6	AX481576 Sequence
13	913.4	97.3	918	6	AX498180 Sequence
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16	907.4	96.6	1499	6	AX288420 Homo sapi
17	690	73.5	972	6	AX451925 Sequence
18	635	67.6	206999	10	AC122886 Mus muscu
19	633.4	67.5	167316	2	AC078995 Mus muscu

20	631.8	67.3	918	10	AY288427	AY288427 Mus muscu
21	524.4	55.8	228766	2	AC099132	AC099132 Rattus no
22	456	48.6	456	9	AY255538	AY255538 Homo sapi
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27	275.2	29.3	393	10	AY255553	AY255553 Mus muscu
28	184	19.6	169155	5	BX088685	BX088685 Zebrafish
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35	76.4	8.1	1113	9	CR542082	CR542082 Homo sapi
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38	76.4	8.1	1805	6	AX746239	AX746239 Sequence
39	76.4	8.1	1973	6	AR270828	AR270828 Sequence
40	76.4	8.1	1973	6	AR380872	AR380872 Sequence
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ALIGNMENTS

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LOCUS AX709193 1336 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 52 from Patent WO02063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G., Kallik,D.A., Ganchi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S., Hafalila,A.D., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R., Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H., Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and Harland,L.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012430CB1"
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Best Local Similarity 99.9%; Pred. No. 2,8e-235;
Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 195 ATGCACAAATGCTACTTCCCAAGTATGCTGGCAATACCTCCAGAAATCTCTTGC 254
QY 61 GATCTATAGTGAACCCCACTTAATACGCTCTTACTATAGTGTATTGCGGGGCTG 120
DB 255 GATCTATAGTGAACCCCACTTAATACGCTCTTACTATAGTGTATTGCGGGGCTG 314
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Db 315 GTGGGCTGATTTTCATTTCTTTCCCTCGTGTAATAATGACACCCGGTCAAGTACACACC 374
Qy 181 ATGGCGGTGATTAATCTTGGTGGTGTCACAGCGTTTTCCTGTCAGTGGCCATTTGCG 240
Db 375 ATGGCGGTGATTAATCTTGGTGGTGTCACAGCGTTTTCCTGTCAGTGGCCATTTGCG 434
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Db 495 GCCATGCTGACATCCACATGTAAGTCAAGTTCCTTCTATGTTGGTGAATCTGTACCC 554
Qy 361 AGATACCTGATCTTCTTCAAGTGCAAGACAAAGTGAATTTTACAGAAAATGTCATGCT 420
Db 555 AGATACCTGATCTTCTTCAAGTGCAAGACAAAGTGAATTTTACAGAAAATGTCATGCT 614
Qy 421 GTGGCTGCGAGTGGTGGCATGTGGAGCGTGGATTTGTCAATGGTACCCCTGGTTGTC 480
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Qy 481 TCCCGGTATGGAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTTCAAGAAAG 540
Db 675 TCCCGGTATGGAATCCATGAGAAATCAATGAGAGACATGTTTAAATTTTCAAGAAAG 734
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RESULT 2
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LOCUS Sequence 53 from Patent WO02063004.
DEFINITION AX709194
ACCESSION AX709194
VERSION AX709194.1 GI:29564788
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
Baughn, M.R., Tibboulley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalik, D.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and

TITLE
JOURNAL
Incyle Genomics, Inc. (US)
FEATURES
source
1. 1340
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyle ID No: 90012586CB1"

ORIGIN
Query Match 98.8%; Score 928.2; DB 6; Length 1340;
Best Local Similarity 99.7%; Pred. No. 7.4e-233;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 AATGTGATCTTCCCAAGTATGCTGGCCACATATACCTCCAGGAATTCCTTGGATCCT 66
Db 205 ACAGGTGATCTTCCCAAGTATGCTGGCCACATATACCTCCAGGAATTCCTTGGATCCT 264
Qy 67 ATATGACACCCCATCTTAATGAGCTTACTTACTTATGATGCTTAATGGGGGCTGGTGGGT 126
Db 265 ATATGACACCCCATCTTAATGAGCTTACTTACTTATGATGCTTAATGGGGGCTGGTGGGT 324
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Db 325 GTCAATTTCAATCTTTCCTCCTGGTGAAGAAATGAACAACCCGGTCAATGACACCATGGCG 384
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Db 445 TACCTCATCAAGAAATGATGATGTTGGGCTGCCCTCTGCAAAATTTGTAGTGCATG 504
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DEFINITION	Sequence 54 from Patent WO02063004.		linear
ACCESSION	AX709195		
VERSION	AX709195.1	GI:29564789	
KEYWORDS			
SOURCE			
ORGANISM			
	Homo sapiens (human)		
REFERENCE			
AUTHORS	1. Baughn, M. R., Tribouley, C. M., Nguyen, D. B., Thornton, M., Yao, M. G., Kalliec, D. A., Gandhi, A. R., Walla, N. K., Arvizu, C., Elliott, V. S., Hatfield, A. J., Ramkumar, J., Pei, J., Tang, Y. T., Yue, H., Reddy, R., Burford, N., Lu, D. A., Graul, R. C., Khan, F. A., Walsh, R. T., Ison, C. H., Richardson, T. W., Griffin, J. A., Warren, B. A., Yang, J., Lee, E. A. and Harland, L.		
TITLE	G-protein coupled receptors		
JOURNAL	Patent: WO 02063004-A 54 15-AUG-2002;		
FEATURES			
source	Incyte Genomics, Inc. (US)		
	Location/Qualifiers		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
	/note="Incyte ID No: 90012670CB1"		
ORIGIN			
Query Match	98.8%; Score 928.2; DB 6; Length 1460;		
Best Local Similarity	99.7%; Pred. No. 7.5e-233;		
Matches	930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	7	AAATGTGACTTCCCAAGTATGCTGTGGCACAATATCTTCAGAAATTCCTCTTGGCATCT	66
Db	325	ACAGTGACTTCCCAAGTATGCTGTGGCACAATATCTTCAGAAATTCCTCTTGGCATCT	384
QY	67	ATAGTGACCCCACTTATAGCCTCTACTTCAATAGTGCTTATTTGGCGGCTGTGGGT	126
Db	385	ATAGTGACCCCACTTATAGCCTCTACTTCAATAGTGCTTATTTGGCGGCTGTGGGT	444
QY	127	GTCATTTCCATCTTTTCTCTGTGTGAATAAGAACCCGGTGACAGTACCAACATGGCG	186
Db	445	GTCATTTCCATCTTTTCTCTGTGTGAATAAGAACCCGGTGACAGTACCAACATGGCG	504
QY	187	GTCATTAAGTGTGTGTGTCCACAGCGCTTTTGTGCTGACAGTGCATTTGGCTGACC	246
Db	505	GTCATTAAGTGTGTGTGTCCACAGCGCTTTTGTGCTGACAGTGCATTTGGCTGACC	564
QY	247	TACCTCATCAAGAAAGCTTGGATGTTTGGCGCTCCCTTGTCAAAATTTGTAGTGCATG	306
Db	565	TACCTCATCAAGAAAGCTTGGATGTTTGGCGCTCCCTTGTCAAAATTTGTAGTGCATG	624
QY	307	CTGACATCCACAGTATACCTGACGTTCTTATATAGTGTGATCTGGTGACAGATAC	366
Db	625	CTGACATCCACAGTATACCTGACGTTCTTATATAGTGTGATCTGGTGACAGATAC	684
QY	367	CTCATCTTTCTTCAAGTGAAGAACAAAGTGAATTTCAACAGAAATCTGCATGCTGTGGCT	426
Db	685	CTCATCTTTCTTCAAGTGAAGAACAAAGTGAATTTCAACAGAAATCTGCATGCTGTGGCT	744
QY	427	GCCAGTGTGGCAATGTGACGCTGTGATTTGTCAATGTGTGTGATACCCCTGTGTGTCTCCCG	486
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QY	487	TATGGAATCCATGAGGAATACAAAGAGAGACACTGTTTAAATTTCCAAAGAGCTTGCT	546
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QY	5447	TACACATATGGAAGAAATCATCAATATATATGATAGCATTTTGTGATAGCGGTGCTGTG	606
Db	865	TACACATATGGAAGAAATCATCAATATATGATAGCATTTTGTGATAGCGGTGCTGTG	924
QY	607	ATTCTGTGTGCTTCCAGGCTTTCATCATATATATGATATGATGAGCAGAAAGCTACGCCACTCT	666
Db	925	ATTCTGTGTGCTTCCAGGCTTTCATCATATATATGATATGATGAGCAGAAAGCTACGCCACTCT	984
QY	667	TTACTATTCACACGAGAGGTTCTGGGCTCAGCTGAAAAAAGCTATTTTATATAGGGGTATC	726
Db	985	TTACTATTCACACGAGAGGTTCTGGGCTCAGCTGAAAAAAGCTATTTTATATAGGGGTATC	1044
QY	727	CTGTGTGTGCTTCCCTCCATCCAGGCTTTCATCATATATATGATATGATGAGCAGAAAGCTACGCCACTCT	786
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QY	787	TCCATATGCTGTAGCAGAGAGTTGCAATTTATATACGAAATCTTCTGAGTGTAAACAGA	846
Db	1105	TCCATATGCTGTAGCAGAGAGTTGCAATTTATATACGAAATCTTCTGAGTGTAAACAGA	1164
QY	847	ATTATGCTGTATGATTTGCTTCTTGTGCTTTGGGGAGAACCATTTGGTTTAAAGCAAAAG	906
Db	1165	ATTATGCTGTATGATTTGCTTCTTGTGCTTTGGGGAGAACCATTTGGTTTAAAGCAAAAG	1224
QY	907	ATAATTTGGCTTATGGAATTTGTTTGTGGCGGT	939
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RESULT 4			
LOCUS	AXI47836	2525 bp	DNA linear PAT 08-JUN-2001
DEFINITION	Sequence 81 from Patent WO0136473.		
ACCESSION	AXI47836		
VERSION	AXI47836.1	GI:14346839	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Enkalyote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Vogeli, G., Wood, L.S., Parodi, L.A., Hiesch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kayes, P.S., Bannigan, C.M., Ruff, V., Seiliez, T. and Huff, R.M.		
JOURNAL	Novel 9 protein-coupled receptors		
FEATURES	Patent: WO 0136473-A 81 25-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)		
source	Location/Qualifiers		
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Query Match	98.8%;	Score 928.2;	DB 6; Length 2525;
Best Local Similarity	99.7%;	Pred. No. 8e-233;	
Matches 930;	Conservative	0; Mismatches	3; Indels 0; Gaps 0;
QY	7	AAATGATCTTCCCAAGATATGCTGGGCACAATACCTCCAGAAATCTCTTGGAGATCT	66
Db	9	ACAGGTACTTCCCAAGATATGCTGGGCACAATACCTCCAGAAATCTCTTGGAGATCT	68
QY	67	ATAATGACACCCCACTTAATACCTCTTACTTATATAGTGTCTTATTTGGCGGGCTGTGGGT	126
Db	69	ATAATGACACCCCACTTAATACCTCTTACTTATATAGTGTCTTATTTGGCGGGCTGTGGGT	128
QY	127	GTCATTTTCATTTCTTTCTCTCGTGGAATAAGAACCCGGGTGATGATACCAACATAGCG	186
Db	129	GTCATTTTCATTTCTTTCTCTCGTGGAATAAGAACCCGGGTGATGATACCAACATAGCG	188

Qy	187	GTGATTAACCTTGGTGTGTGTCCACAGCGTTTTTCTGTCTGACAGTGTCCATTTGCTTGAAC	246
Db	189	GTGATTAACCTTGGTGTGTGTCCACAGCGTTTTTCTGTCTGACAGTGTCCATTTGCTTGAAC	248
Qy	247	TACCTCATCAAGAAGACTTGGAGTTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATG	306
Db	249	TACCTCATCAAGAAGACTTGGAGTTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATG	308
Qy	307	CTGCACATCCACATGTACTTCGATCGTTCCATATTTATATGTGTGATCTGTGTCCACAGATAC	366
Db	309	CTGCACATCCACATGTACTTCGATCGTTCCATATTTATGTGTGATCTGTGTCCACAGATAC	368
Qy	367	CTCAATCTCTTCAAGTGTGAAGAACAATGTGAATTTCTACAAAACTGCATGCTGTGCT	426
Db	369	CTCAATCTCTTCAAGTGTGAAGAACAATGTGAATTTCTACAAAACTGCATGCTGTGCT	428
Qy	427	GCCAGTGTGTGCATGTGAGACGCTGTGTGATTTGTCAATTTGTGTATCCCTGTGTCTCCGG	486
Db	429	GCCAGTGTGTGCATGTGAGACGCTGTGTGATTTGTCAATTTGTGTATCCCTGTGTCTCCGG	488
Qy	487	TATGGAATCCATGAGAAATACATGAGAGACACTGTTTTAAATTTACAAAAGACTTGCT	546
Db	489	TATGGAATCCATGAGAAATACATGAGAGACACTGTTTTAAATTTACAAAAGACTTGCT	548
Qy	547	TACACATATGTGAAAATATCATCAATATGTATGATGATGTGACAGAACTACGCACTCT	606
Db	549	TACACATATGTGAAAATATCATCAATATGTATGATGATGTGATGACAGAACTACGCACTCT	608
Qy	607	ATTCTGTTGTGCTTCCAGGTCTTCATCATATATGTGATGTGACAGAACTACGCACTCT	666
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Qy	727	CTGTGTTGTTCCTTCCCTACACAGTTCTTATGGAATCTATPACTTGAATGTGTGACGCAT	786
Db	729	CTGTGTTGTTCCTTCCCTACACAGTTCTTATGGAATCTATPACTTGAATGTGTGACGCAT	788
Qy	787	TCCAAATGCTGTAGCAGCAGAGTTGCATTTATTAACGAATCTTCTTGAGTGTAAACAGA	846
Db	789	TCCAAATGCTGTAGCAGCAGAGTTGCATTTATTAACGAATCTTCTTGAGTGTAAACAGA	848
Qy	847	ATTAGCTGTCTATGATTTTGCTTCTCTTTGTCTTTGGGGGAACCAATGTTTAAAGCAAAAG	906
Db	849	ATTAGCTGTCTATGATTTTGCTTCTCTTTGTCTTTGGGGGAACCAATGTTTAAAGCAAAAG	908
Qy	907	ATTAATTTGGCTTATGGAATTGTGTTTGTGGCGT	939
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LOCUS	Sequence 81 from Patent WO02064789.	linear	PAT 24-OCT-2002
DEFINITION	AX521885		
ACCESSION	AX521885.1		
VERSION	AX521885.1		
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Lind, P., Parodi, L.A., Vogel, G. and Wood, L.S.		
TITLE	G protein-coupled receptor		
JOURNAL	Patent: WO 02064789-A 81 22-AUG-2002;		
	PHARMACIA & UPJOHN COMPANY (US)		
FEATURES	Location/Qualifiers		
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QY	7	AAATGTGACTTCCCAAGTATGCTTGGCCCAACAATCTTCAGAGAATCTCTTGGCATCTCT	66		
DB	9	ACAGGTGACTTCCCAAGTATGCTTGGCCCAACAATCTTCAGAGAATCTCTTGGCATCTCT	68		
QY	67	ATTAGTACACCCCACTTATCAGCCTCTACTCTTATAGTCTTATTTGCGGCTGGTGGGT	126		
DB	69	ATTAGTACACCCCACTTATCAGCCTCTACTCTTATAGTCTTATTTGCGGCTGGTGGGT	128		
QY	127	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGGTCACTGATCAACCATGCGC	186		
DB	129	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGGTCACTGATCAACCATGCGC	188		
QY	187	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGGTCACTGATCAACCATGCGC	246		
DB	189	GTCATTTTCATTTCTTCTCTCTGAGAAATGAACACCCGGTCACTGATCAACCATGCGC	248		
QY	247	TACCTCATCAAGAAGACTTGGATGTTGGGCTGGCCCTCTGCAATTTGTGAGTGCATG	306		
DB	249	TACCTCATCAAGAAGACTTGGATGTTGGGCTGGCCCTCTGCAATTTGTGAGTGCATG	308		
QY	307	CTGCACATCCACATGATACCTGACGTTCTTATTTATGTTGATCTCTGTCACAGATAC	366		
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QY	367	CTCATCTCTCTTCAAGTGCAGAAACAAAGTGAATTTCTACAGAAAACCTCATGCTGGCT	426		
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QY	427	GCCAGTGTGCATGTGTGACGCTGAGTGTGTCAATTTGTGTACCCCTGGTGTCTCCCGG	486		
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QY	487	TATGAAATCCATGAGAGAAATCAATGAGAGACAGCTTTTAAATTTCACAAAAGGCTTGC	546		
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QY	547	TACACATATGTGAATAATCATCACTATATGATGATCTTTTGTGATACCGCTTCTG	606		
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QY	607	ATTCTGTGTGCTTCCAGTCTTCACTATATTTATGTTGATGTTGAGAGACTTACGCCACT	666		
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QY	667	TTACTATCCCAACAGAGATTCTGGGCTCAGCTGAAAAAATCTATTTTATAGGGGTCTATC	726		
DB	669	TTACTATCCCAACAGAGATTCTGGGCTCAGCTGAAAAAATCTATTTTATAGGGGTCTATC	728		
QY	727	CTGTGTGTCTTCTTCCCTACAGTCTTATAGATCTATTTAATCTTGAATGTTGTGACGAT	786		
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QY	787	TCCATATGCTGTAGAGAGAGAGTTCATTTATACGAAATCTTCTTATAGTGTAAACACA	846		
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QY	847	ATTAGTGTGTATGATTTGCTTCTTGTGTCTTTTGGGGAGAACCAATGTTTAAAGCAAAAG	906		
DB	849	ATTAGTGTGTATGATTTGCTTCTTGTGTCTTTTGGGGAGAACCAATGTTTAAAGCAAAAG	908		
QY	907	ATTATGTGCTTATGGAATTTGTTTGTGTGCGCT 939			
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LOCUS	AX646815	113306 bp	DNA	linear	PAT 04-MAR-2003
DEFINITION	Sequence 1007 from Patent EP1270724.				
ACCESSION	AX646815				
VERSION	AX646815.1	GI:28799225			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
JOURNAL	1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H. Guanoine triphosphate-binding protein coupled receptors Patent: EP 1270724-A 1007 02-JAN-2003; National Institute of Advanced Industrial Science and Technology (JIP) / Center for Advanced Science and Technology Incubation, Ltd. (JIP)				
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Query Match	98.8%; Score 927.8; DB 6; Length 113306;				
Best Local Similarity	99.8%; Pred. No. 1.6e-222;				
Matches 929; Conservative	0; Mismatches 2; Indels 0; Gaps 0;				
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Db	11944	CAGTGTGGCAGATGTGACGCTGGTGATTTGTCATTTGTGTGATACCCCTGGTGTCTCCGAGTA	1200
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QY	669	ACTATCCACACAGAGATTTCTGGGCTCAGCTGAAACCTATTTTATATAGGGGTCACTCT	728
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QY	729	TGTTTGTTCCTTCCCTACCAAGTCTTTAGATCTATTTACTGATGTTGTGACGATTC	788
Db	12244	TGTTTGTTCCTTCCCTACCAAGTCTTTAGATCTATTTACTGATGTTGTGACGATTC	1230
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DEFINITION			Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION	AC083865		
VERSION	AC083865.2	GI:12545315	
KEYWORDS			HTG.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS			1 (bases 1 to 218186)
			Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.
TITLE			Large-scale Mapping and Sequencing of Human Chromosome 7
JOURNAL			Unpublished
REFERENCE			2 (bases 1 to 218186)
AUTHORS			Kaul, R., Olson, M.V., Raymond, C., Clendinning, J. and Haugen, E.
JOURNAL			Direct Submission
			Submitted (04-OCT-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
			3 (bases 1 to 218186)
REFERENCE			Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.
AUTHORS			Direct Submission
TITLE			Submitted (26-JAN-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL			On Jan 26, 2001 this sequence version replaced gi:10567930.
COMMENT			----- Genome Center
			Center: University of Washington Genome Center
			Center Code: UMG
			Web site: http://www.genome.washington.edu
			Contact: uwgchgs@u.washington.edu
			----- Project Information
			Center project name: HsaChr7
			Center clone name: RP11-605P22 (dj5708)
			----- Summary Statistics
			Sequencing vector: Plasmid; X52328; 100% of reads

Chemistry: Dye-terminator ET-amerham; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 217693 bases at least Q40
 Consensus quality: 218145 bases at least Q30
 Consensus quality: 218186 bases at least Q20
 Insert size: 273875; 19.1% error; agarose-fp
 Insert size: 218186; sum-of-contrigs
 Quality coverage: 8.30x in Q20 bases; agarose-fp
 Quality coverage: 10.42x in Q20 bases; sum-of-contrigs

Overlapping Sequences:

5': mapping in progress
 3': RP11-243B12 (UMGC:djs156) AC018634, 6468-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap FngPrnt

SeqDerMap FngPrnt

SeqDerMap FngPrnt

SeqDerMap FngPrnt

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4508	4455	4273	4301	324	<800
5815	5686	1980	2031	1496	1421
5380	5309	520	<800	6710	6637
349	<800	737	755	71	<800
4509	4612	1833	1878	848	877
571	<800	8798	8985	6153	6135
4162	4455	2024	2031	4085	4113
956	988	4946	4869	14	<800
2026	2123	6247	6163	44	<800
1821	1788	685	<800	10402	10360
2453	2471	1367	1406	300	<800
8955	9499	109	<800	5150	5294
1004	988	3608	3535	3195	3246
7399	7468	7728	7736	2281	2309
7516	7468	4264	4301	2740	2804
4119	4107	357	<800	5869	5921
193	<800	3645	3709	248	<800
2792	2805	1961	2031	3072	3079
7034	7468	5668	5588	585	<800
4940	4902	957	918	655	<800
603	<800	5024	4869	1206	1270

		761	<800	201	<800	1723	1693
		2518	2471	1119	1195	19721	20141
		4086	4107	709	<800	2331	2309
		5916	5835	4907	4869	1940	1993
		6995	6947	1161	1195	5574	5585
		4667	4612	11292	11329	3867	3865
		10434	10231	6699	6611	1268	1270
		1306	1313	1358	1406	8347	8084
		374	<800	2400	2394	3636	3640
Query Match	98.8%;	Score 927.8;	DB 9;	Length 218186;			
Best Local Similarity	99.8%;	Pred. No. 1.7e-232;					
Matches 929;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;			
QY	9	ATGTGACTTCCAGATAGTGCCTG3CCACATACCTCCAGGAATTCCTTGCCATCCTAT	68				
DB	133107	AGGTGACTTCCAGATAGTGCCTG6CCACATACCTCCAGGAATTCCTTGCCATCCTAT	133166				
QY	69	AGTGAACCCCACTTAATACGCTCTTACTATAGTGTCTTATTTGGCGG9GTGTGT	128				
DB	133167	AGTGAACCCCACTTAATACGCTCTTACTATAGTGTCTTATTTGGCGG9GTGTGT	133226				
QY	129	CATTTCATCTTCTTCTCTCTGTAAGAAACACCCGCTCAGTACCCACATGCGGT	188				
DB	133227	CATTTCATCTTCTTCTCTCTGTAAGAAACACCCGCTCAGTACCCACATGCGGT	133286				
QY	189	CATTAACTGTGTGTGTGTGCACAGCGTTTTCGTGTGACAGTCCATTCGTTGACCTA	248				
DB	133287	CATTAACTGTGTGTGTGTGCACAGCGTTTTCGTGTGACAGTCCATTCGTTGACCTA	133346				
QY	249	CCTCATCAGAGACCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCCATGCT	308				
DB	133347	CCTCATCAGAGACCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCCATGCT	133406				
QY	309	GCAATCCACATATACCTGACGTTTCCATTTCTATGTGTGTATCTGTGTGACCGATACCT	368				
DB	133407	GCAATCCACATATACCTGACGTTTCCATTTCTATGTGTGTATCTGTGTGACCGATACCT	133466				
QY	369	CATCTTCTTCAAGTGAAGACAAAGTGAATTTCTACAGAAAAGTGCATGCTGTGCTGC	428				
DB	133467	CATCTTCTTCAAGTGAAGACAAAGTGAATTTCTACAGAAAAGTGCATGCTGTGCTGC	133526				
QY	429	CAGTGTGTGATGTGACGCTGTGTGTGTCTATGTGTGTATCCCTGTGTGTCTCCCGGTA	488				
DB	133527	CAGTGTGTGATGTGACGCTGTGTGTGTCTATGTGTGTATCCCTGTGTGTCTCCCGGTA	133586				
QY	489	TGGAATCCATGAGGATTAATGAGAGACGCTGTTTAAATTTCAAGAAAGCTTGCTTA	548				
DB	133587	TGGAATCCATGAGGATTAATGAGAGACGCTGTTTAAATTTCAAGAAAGCTTGCTTA	133646				
QY	549	CACATATGGAAGAAATCATCAATATATGATGATGTTTGTGATGCGGTGTGCTGTAT	608				
DB	133647	CACATATGGAAGAAATCATCAATATATGATGATGTTTGTGATGCGGTGTGCTGTAT	133706				
QY	609	TCTGTGTGCTTTCAGGTCTTCAATATATGTTGATGTGTGACAGAGCTACGCCACTT	668				
DB	133707	TCTGTGTGCTTTCAGGTCTTCAATATATGTTGATGTGTGACAGAGCTACGCCACTT	133766				
QY	669	ACATATCCACAGAGATTTCTGGGCTCAGCTGAAAGAACTATTTTATAGGGGTCACTCT	728				
DB	133767	ACATATCCACAGAGATTTCTGGGCTCAGCTGAAAGAACTATTTTATAGGGGTCACTCT	133826				
QY	729	TGTTGTCTTCTTCCCTACAGTTCTTTAGATCTATTAAGATGTTGTGACGATTC	788				

DB	133827	TGTTGTCTTCTTCCCTACAGTTCTTTAGATCTATTAAGATGTTGTGACGATTC	133886				
QY	789	CAATGCTGTGACAGAGAGTTGCATTTTATTAAGAAATCTTTGATGTAAACAGCAAT	848				
DB	133887	CAATGCTGTGACAGAGAGTTGCATTTTATTAAGAAATCTTTGATGTAAACAGCAAT	133946				
QY	849	TACGTGTATGATTTGCTTCTTGTCTTTGGGGAGAGCATGTGTTTAAGAAAAGAT	908				
DB	133947	TACGTGTATGATTTGCTTCTTGTCTTTGGGGAGAGCATGTGTTTAAGAAAAGAT	134006				
QY	909	AATTGCTTATGGAATTTGTTTGTGCGGT	939				
DB	134007	AATTGCTTATGGAATTTGTTTGTGCGGT	134037				
RESULT 8							
LOCUS	C0737895	1332 bp	DNA	linear	PAT 03-FEB-2004		
DEFINITION	Sequence 23829 from Patent WO02068579.						
ACCESSION	C0737895						
VERSION	C0737895.1	GI:42337355					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE 1	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.						
AUTHORS	Kite, such as nucleic acid arrays, comprising a majority of						
TITLE	humexons or transcripts, for detecting expression and other uses						
JOURNAL	Patent: WO 02068579-A 23829 06-SEP-2002;						
FEATURES	PE Corporation (NY) (US)						
source	1..1332						
ORIGIN							
Query Match	98.8%;	Score 927.4;	DB 6;	Length 1332;			
Best Local Similarity	99.9%;	Pred. No. 1.2e-232;					
Matches 928;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;			
QY	11	GTGACTTCCAGATATGCTGTGCGCACATATCTCCAGAAATTCCTTGCATATAG	70				
DB	401	GTGACTTCCAGATATGCTGTGCGCACATATCTCCAGAAATTCCTTGCATATAG	460				
QY	71	TGACACCCCACTTAATCAAGCTCTTACTATAGTGTCTTATTTGGCGGCTGTGGGTGTA	130				
DB	461	TGACACCCCACTTAATCAAGCTCTTACTATAGTGTCTTATTTGGCGGCTGTGGGTGTA	520				
QY	131	TTTCCATCTTCTTCCCTGTAAGAAATGAACCCGCGTCACTGACACCATGGCGGTCA	190				
DB	521	TTTCCATCTTCTTCCCTGTAAGAAATGAACCCGCGTCACTGACACCATGGCGGTCA	580				
QY	191	TTAACTGTGTGTGTGTCACAGCGTTTCTGTCTGACAGTGCATTTGCTTGACCTACC	250				
DB	581	TTAACTGTGTGTGTGTCACAGCGTTTCTGTCTGACAGTGCATTTGCTTGACCTACC	640				
QY	251	TGATCAAGAAAGCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCGATGCTGC	310				
DB	641	TGATCAAGAAAGCTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCGATGCTGC	700				
QY	311	ACATCCACATGATACCTCAGGTTCTATTTCTATGTGTGTGCTGTGACAGATACCTCA	370				
DB	701	ACATCCACATGATACCTCAGGTTCTATTTCTATGTGTGTGCTGTGACAGATACCTCA	760				
QY	371	TCTTCTTCAAGTGAAGACAAAGTGAATTTCTACAGAAAAGTGCATGTGTGTGCGCA	430				
DB	761	TCTTCTTCAAGTGAAGACAAAGTGAATTTCTACAGAAAAGTGCATGTGTGTGCGCA	820				
QY	431	GTCTGTGACATGTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	490				

|||||
Db 821 GAGCTGGCAGTNGACGCTGTGATGTGATGTGTGTAACCCCTGGTGTGCTCCCGGTATG 880
Qy 491 GAATCATATGAGAAATCAATGAGAGACACTGTTTAAATTTTCACAAAGAGCTTGCTTAA 550
Db 881 GAATCATATGAGAAATCAATGAGAGACACTGTTTAAATTTTCACAAAGAGCTTGCTTAA 940
Qy 551 CATATGAAAAATCATCACTATATGATAGTCAATTTTGTGATAGCCGTGCTGTGATTC 610
Db 941 CATATGAAAAATCATCACTATATGATAGTCAATTTTGTGATAGCCGTGCTGTGATTC 1000
Qy 611 TGTGTGCTTCCAGGCTTTCATCATATGTTGATGTGAGAGAAAGCTACGCCACTTTTAC 670
Db 1001 TGTGTGCTTCCAGGCTTTCATCATATGTTGATGTGAGAGAAAGCTACGCCACTTTTAC 1060
Qy 671 TATCCACACAGAGATCTGAGGCTCAGCTGAAAAAACCCTATTTTAAAGAGGTCATCCCTG 730
Db 1061 TATCCACACAGAGATCTGAGGCTCAGCTGAAAAAACCCTATTTTAAAGAGGTCATCCCTG 1120
Qy 731 TTTGTTCCCTCCCTACCAATCTTATAGATCTATTAATTAATGTTGATGACGATTTCA 790
Db 1121 TTTGTTCCCTCCCTACCAATCTTATAGATCTATTAATTAATGTTGATGACGATTTCA 1180
Qy 791 ATGCTGTAGACAGAGATTTGATTTTATACGAAATCTTCTTACGTGTACAGCAATTA 850
Db 1181 ATGCTGTAGACAGAGATTTGATTTTATACGAAATCTTCTTACGTGTACAGCAATTA 1240
Qy 851 GGTGCTATAGATTTGCTCTCTTGTGTTGGGGAGAGCAATGTTAAGCAAAATATA 910
Db 1241 GGTGCTATAGATTTGCTCTCTTGTGTTGGGGAGAGCAATGTTAAGCAAAATATA 1300
Qy 911 TTGGCTTATGAAATGTGTTTGTGCGGT 939
Db 1301 TTGGCTTATGAAATGTGTTTGTGCGGT 1329

RESULT 9
AX453412 1051 bp DNA linear PAT 06-JUL-2002
LOCUS AX453412
DEFINITION Sequence 1 from Patent WO0244212.
ACCESSION AX453412
VERSION AX453412.1 GI:21712725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Deleersnijder, W., Blockx, H. and de Moor, L.
JOURNAL Human g-protein coupled receptor and uses thereof
Patent: WO 0244212-A 1 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
source location/Qualifiers
1..1051
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
60..977
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38106.1"
/db_xref="GI:21712726"
/translation="MPGNTSRNSCDPIVTPHLISLVEPIVLIGGLVGVISILFLVK
NMTBSVTMAVINLVVHSVPLITVPEFLRLIILKTMWGLPCKKSVSAMLHMYLT
PLPYVILITRLILPFKCDKREPKLHAVAASGMTLVIVIVPLVVSXGHEE
YNEBHFKEHLATYTKIINMIVIFIAVAIVLVQVFIIMLVOKLHSLISH
QEPWQKNLFFIQLVCFPLVQFRIYLVVTHSNCSKVAFYMEIFLSVTAIS
CYDLLLFVFGSHWFKQIIGMNCVLCR"
ORIGIN
Query Match 98.6%; Score 926.2; DB 6; Length 1051;
Best Local Similarity 99.7%; Pired. No. 2.4e-232;
Matches 928; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ATGTGACCTTCCCAAGTATGCTGGCCACAAATPACTCCAGAAATTCCTTGGGATCTAT 68
Db 44 AGGTGACCTTCCCAAGTATGCTGGCCACAAATPACTCCAGAAATTCCTTGGGATCTAT 103
Qy 69 AGTGAACCCCACTTAATCAGCTTACTTCACTAGTCTTATTTGGCGGGCTGGGGTGT 128
Db 104 AGTGAACCCCACTTAATCAGCTTACTTCACTAGTCTTATTTGGCGGGCTGGGGTGT 163
Qy 129 CATTTCCATTTCTTTCTCCCTGGTGAATAAGAACCCGGTCAAGTACACACATGGCGGT 188
Db 164 CATTTCCATTTCTTTCTCCCTGGTGAATAAGAACCCGGTCAAGTACACATGGCGGT 223
Qy 189 CATTAATTTGGTGTGTTCACAGAGGTTTTCCTGTGACAGTGCATTTGCTTACCTTA 248
Db 224 CATTAATTTGGTGTGTTCACAGAGGTTTTCCTGTGACAGTGCATTTGCTTACCTTA 283
Qy 249 CCTCATCAAGAAAGCTTGGATGTTTGGGCTGCTCTTTCGAAATTTGTGATGTCATGCT 308
Db 284 CCTCATCAAGAAAGCTTGGATGTTTGGGCTGCTCTTTCGAAATTTGTGATGTCATGCT 343
Qy 309 GCACATCCACATGTACCTTCAGTTCCTATTCATATGTTGATTCCTGTGTACAGATACCT 368
Db 344 GCACATCCACATGTACCTTCAGTTCCTATTCATATGTTGATTCCTGTGTACAGATACCT 403
Qy 369 CATTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCTGC 428
Db 404 CATTTCTTCAAGTGCAAAGACAAAGTGAATTTCTACAGAAATTCGATGCTGTGGCTGC 463
Qy 429 CAGTCTGGCATGTGACGCTGTGTGATTTGTGATGTTGATGTCATGCTGTGTGCTCCGGTA 488
Db 464 CAGTCTGGCATGTGACGCTGTGTGATTTGTGATGTTGATGTCATGCTGTGTGCTCCGGTA 523
Qy 489 TGGAAATCCATGAGAAATCAATGAGAGACGTTTAAATTTCACAAAGCTTGCTTA 548
Db 524 TGGAAATCCATGAGAAATCAATGAGAGACGTTTAAATTTCACAAAGCTTGCTTA 583
Qy 549 CACATATGTGAATAATCATCACTATATGATAGTCAATTTTGTGATAGCGCTGTGTGAT 608
Db 584 CACATATGTGAATAATCATCACTATATGATAGTCAATTTTGTGATAGCGCTGTGTGAT 643
Qy 609 TCTGTTGGCTTTCAGGCTTCTCATATTAATGTTGATGTTGATGTTGATGTTGATGTTG 668
Db 644 TCTGTTGGCTTTCAGGCTTCTCATATTAATGTTGATGTTGATGTTGATGTTGATGTTG 703
Qy 669 ACTATCCACACAGAGTCTGGGCTCAGCTGAAAACCTATTTTAAAGGGTCACTCT 728
Db 704 ACTATCCACACAGAGTCTGGGCTCAGCTGAAAACCTATTTTAAAGGGTCACTCT 763
Qy 729 TGTGTTGTTCCCTCCCTACCAAGTCTTTAAGATCTATTAATGTTGATGACCATTC 788
Db 764 TGTGTTGTTCCCTCCCTACCAAGTCTTTAAGATCTATTAATGTTGATGACCATTC 823
Qy 789 CAATGCTGTAGACAGCAAGTTCATTTTATACGAAATCTTCTTGAAGTGAACGCAAT 848
Db 824 CAATGCTGTAGACAGCAAGTTCATTTTATACGAAATCTTCTTGAAGTGAACGCAAT 883
Qy 849 TAGCTGTATGATTTGCTTCTCTTGTGTTGGGGAGAGCAATGTTAAGCAAAAGT 908
Db 884 TAGCTGTATGATTTGCTTCTCTTGTGTTGGGGAGAGCAATGTTAAGCAAAAGT 943
Qy 909 AATGCTTATGAAATGTGTTTGTGCGGT 939
Db 944 AATGCTTATGAAATGTGTTTGTGCGGT 974
RESULT 10
AC146385 162268 bp DNA linear PRI 19-MAY-2004
LOCUS AC146385
DEFINITION Pan troglodytes BAC clone RP43-126C6 from 7, complete sequence.
ACCESSION AC146385
VERSION AC146385.4 GI:46391241
KEYWORDS HTG.

RESULT 11
BD187510

LOCUS BD187510 918 bp DNA linear PAT 17-JUL-2003

DEFINITION Novel Polypeptide.

ACCESSION BD187510.1 GI:32997249

VERSION JP 2003024082-A/1.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 918)
Lee, H.
Novel Polypeptide
Patent: JP 2003024082-A 1 28-JAN-2003;
Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)

COMMENT OS Homo sapiens
PN JP 2003024082-A/1
PD 28-JAN-2003
PE 17-JAN-2002 JP 2002008881
PR 23-JAN-2001 GB 0101739.1
PI Harland Lee
CC

FEATURES
source 1..918
Location/Qualifiers.
Key Location/Qualifiers.
1..918
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 97.3%; Score 913.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 5.5e-229;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

25 ATGCGTGGCCACAAATACCTTCAGAAATTCCTTCGATCTCTAATAGTGAACCCCACTTA 84
1 ATGCGTGGCCACAAATACCTTCAGAAATTCCTTCGATCTCTAATAGTGAACCCCACTTA 60

QY 85 ATCAGGCTCTACTTCAATAGTGCCTTATGCGGGCTGTGGGGTCAATTCCTTCTTTTC 144
DB 61 ATCAGGCTCTACTTCAATAGTGCCTTATGCGGGCTGTGGGGTCAATTCCTTCTTTTC 120

QY 145 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGCGGTCAATTAATCTTGATG 204
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGCGGTCAATTAATCTTGATG 180

QY 205 GTCCACAGCGTTTTCGTGACAGTGCATTTCCGCTTGACCTTCACTCAAGAACT 264
DB 181 GTCCACAGCGTTTTCGTGACAGTGCATTTCCGCTTGACCTTCACTCAAGAACT 240

QY 265 TGGATGTTGGGCTGCCCTTCGCAAAATTTGGAAGTGCATGCTGACATCCACATGTAC 324
DB 241 TGGATGTTGGGCTGCCCTTCGCAAAATTTGGAAGTGCATGCTGACATCCACATGTAC 300

QY 325 CTCAGCTTCTATTCTATGAGTGCCTGTGACCAAGTACCTCATCTTCTCAAGTAC 384
DB 301 CTCAGCTTCTATTCTATGAGTGCCTGTGACCAAGTACCTCATCTTCTCAAGTAC 360

QY 385 AAAGCAAAAGTGAATTCACAGAAAATGCAATGCTGTGGCTGCCAGTCTGGCATGTG 444
DB 361 AAAGCAAAAGTGAATTCACAGAAAATGCAATGCTGTGGCTGCCAGTCTGGCATGTG 420

QY 445 AGCGTGTGATTTGCTATGTTGGTACCCCTGTGTTGTCTCCCGTATGGAATCCATGAGAA 504
DB 421 AGCGTGTGATTTGCTATGTTGGTACCCCTGTGTTGTCTCCCGTATGGAATCCATGAGAA 480

QY 505 TCAATGAGAGAGACGTTTAAATTTCAAAAGAGCTTGCTTACACATATGGAATTC 564
DB 481 TCAATGAGAGAGACGTTTAAATTTCAAAAGAGCTTGCTTACACATATGGAATTC 540

QY 565 ATCAACTATATAGTATGATCTTTTGTGCATAGCCGTGCTGTGATTCGTGTGCTTCCAG 624
DB 541 ATCAACTATATAGTATGATCTTTTGTGCATAGCCGTGCTGTGATTCGTGTGCTTCCAG 600

QY 625 GTTCTCATCATTTATGTTGATGTGACAGAAAGCTACGCCACTGTTTACTATCCACAGAG 684
DB 601 GTTCTCATCATTTATGTTGATGTGACAGAAAGCTACGCCACTGTTTACTATCCACAGAG 660

QY 685 TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGTCATCCTGTTGTTCCCTCC 744
DB 661 TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGTCATCCTGTTGTTCCCTCC 720

QY 745 TACAGATCTTTAGATCTTATTCTTGAATGTTGACGCAATTCGAATGCTGTAGCAGC 804
DB 721 TACAGATCTTTAGATCTTATTCTTGAATGTTGACGCAATTCGAATGCTGTAGCAGC 780

QY 805 AAGTTGCACTTTTAAAGAAATCTTTCTGAGTGTAAACAGAAATAGCTGTATGATTTG 864
DB 781 AAGTTGCACTTTTAAAGAAATCTTTCTGAGTGTAAACAGAAATAGCTGTATGATTTG 840

QY 865 CTTCCTTTGCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATTAATTGCTTATGAAAT 924
DB 841 CTTCCTTTGCTTTGGGGGAAGCCATTTGTTAAGCAAAAGATTAATTGCTTATGAAAT 900

QY 925 TGTGTTTGTGCGGT 939
DB 901 TGTGTTTGTGCGGT 915

RESULT 12
AX481576 918 bp DNA linear PAT 16-AUG-2002
AX481576
DEFINITION Sequence 1 from Patent EP1225183.
ACCESSION AX481576
VERSION AX481576.1 GI:22316490

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Harland, L.
Human g-protein coupled receptor
Patent: EP 1225183-A 1 24-JUL-2002;
Pfizer Limited (GB) ; PFIZER INC. (US)

FEATURES
source 1..918
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 97.3%; Score 913.4; DB 6; Length 918;
Best Local Similarity 99.9%; Pred. No. 5.5e-229;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

25 ATGCGTGGCCACAAATACCTTCAGAAATTCCTTCGATCTCTAATAGTGAACCCCACTTA 84
1 ATGCGTGGCCACAAATACCTTCAGAAATTCCTTCGATCTCTAATAGTGAACCCCACTTA 60

QY 85 ATCAGGCTCTACTTCAATAGTGCCTTATGCGGGCTGTGGGGTCAATTCCTTCTTTTC 144
DB 61 ATCAGGCTCTACTTCAATAGTGCCTTATGCGGGCTGTGGGGTCAATTCCTTCTTTTC 120

QY 145 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGCGGTCAATTAATCTTGATG 204
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGCGGTCAATTAATCTTGATG 180

QY 205 GTCCACAGCGTTTTCGTGACAGTGCATTTCCGCTTGACCTTCACTCAAGAACT 264
DB 181 GTCCACAGCGTTTTCGTGACAGTGCATTTCCGCTTGACCTTCACTCAAGAACT 240

QY 265 TGGATGTTGGGCTGCCCTTCGCAAAATTTGGAAGTGCATGCTGACATCCACATGTAC 324

Db	241	TGGATGTTTGGGCTGCCCTCTTCGCAAAATTGAGTGGCACTGCAATCCAAATGAC	300
Qy	325	CTCAGGTTTCCTAATTCATGTGATGTGATCCTGGTCACACAGATACCTCATCTTCTTCAAGTGC	384
Db	301	CTCAGGTTCTCTAATTCATGTGATGTGATCCTGGTCACACAGATACCTCATCTTCTTCAAGTGC	360
Qy	385	AAAGCAAAATGTGGAATTTCTACAGAAAACATGCATGCTGTGAGCTGCCAGTCTGGCATGTGG	444
Db	361	AAAGCAAAATGTGGAATTTCTACAGAAAACATGCATGCTGTGAGCTGCCAGTCTGGCATGTGG	420
Qy	445	ACGCTGTGATATGTGCTATTTGTGGNACCCCGTGTTGTCTCCCGGATATGGAATCCATAGGAA	504
Db	421	ACGCTGTGATATGTGCTATTTGTGGNACCCCGTGTTGTCTCCCGGATATGGAATCCATAGGAA	480
Qy	505	TACAAATGAGAGCACTGTTTTAAATTTCAAAAGACTGTCTTACACATATGTGAAAATC	564
Db	481	TACAAATGAGAGCACTGTTTTAAATTTCAAAAGACTGTCTTACACATATGTGAAAATC	540
Qy	565	ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTTCTGTGGTCTTCCAG	624
Db	541	ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTTCTGTGGTCTTCCAG	600
Qy	625	GTCCTCATCATATGATGTGATGTGGAGAGAGCTAGCCCACTCTTTACTATATCCACAGAGAG	684
Db	601	GTCCTCATCATATGATGTGATGTGGAGAGAGCTAGCCCACTCTTTACTATATCCACAGAGAG	660
Qy	685	TTCTGGGGCTCAAGCTGAAAAACCTAATTTTTATAGGGGTCATCCTGTGTTGTTCTCTCC	744
Db	661	TTCTGGGGCTCAAGCTGAAAAACCTAATTTTTATAGGGGTCATCCTGTGTTGTTCTCTCC	720
Qy	745	TACCACTTCTTAAAGATCTAATTACTTGAATGTTGTGACGCAATCCAAATGCTTAGACAGC	804
Db	721	TACCACTTCTTAAAGATCTAATTACTTGAATGTTGTGACGCAATCCAAATGCTTAGACAGC	780
Qy	805	AAGGTGCAATTTATATAGCAAAATCTCTTGACTGTAAACAGCAATTAAGCTGCTATGATTTG	864
Db	781	AAGGTGCAATTTATATAGCAAAATCTCTTGACTGTAAACAGCAATTAAGCTGCTATGATTTG	840
Qy	865	CTTCTCTTCTTGTCTTTGGGGAAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTAGTAAT	924
Db	841	CTTCTCTTCTTGTCTTTGGGGAAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTAGTAAT	900
Qy	925	TGTGTTTTGTGCGGT	939
Db	901	TGTGTTTTGTGCGGT	915
RESULT 13			
LOCUS	AX498180	918 bp	DNA
DEFINITION	Sequence 3 from Patent WO0242461.	linear	PAT 26-SEP-2002
ACCESSION	AX498180		
VERSION	AX498180.1	GI:23343111	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	Chen, R., Chu, Z.L., Dang, H.T., Lowitz, K.P. and Pride, C.		
AUTHORS	1		
TITLE	Endogenous and non-endogenous versions of human g protein-coupled		
	receptors		
JOURNAL	Patent: WO 0242461-A 3 30-MAY-2002;		
	Arena Pharmaceuticals, Inc. (US)		
FEATURES	location/Qualifiers		
source	1..918		
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	/db_xref="taxon:9606"		
ORIGIN			
Query Match	97.3%;	Score 913.4;	DB 6; Length 918;

[illegible]

VERSION BD105324.1 GI:22650898
KEYWORDS MO 0196567-A/1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.
TITLE Novel G protein-coupled receptor protein and its DNA
JOURNAL Patent: WO 0196567-A 1 20-DEC-2001.
TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
COMMENT OS Homo sapiens (human)
PN MO 0196567-A/1
PD 20-DEC-2001
PF 14-JUN-2001 WO 2001JP005061
PR 15-JUN-2000 JP 00P 194596,19-JUL-2000 JP 00P 223887 PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00,
PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC
A61P29/00,
PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/53, G01N33/566//
PC (C12N1/21, C12R1:19), (C12P21/02, C12R1:19)
CC Novel G protein-coupled receptor protein and its DNA FH Key
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DEFINITION Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete cds.
ACCESSION AY288420
VERSION AY288420.1 GI:32165523
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 918)
Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and
Schioth,H.B.
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled
receptors lacking close relatives
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)
MEDLINE 22985413
PUBMED 14623098

REFERENCE 2 (bases 1 to 918)
Fredriksson,R., Hoglund,P.J., Gloriam,D.E.I., Lagerstrom,M.C. and
Schioth,H.B.
TITLE Direct Submision
JOURNAL Submitted (30-Apr-2003) Neuroscience; Unit of Pharmacology, Uppsala
University, Box 593, Uppsala 75124, Sweden
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Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AA153414 standard; DNA; 939 BP.

AA153414;

12-DEC-2002 (first entry)

939 nt coding DNA of a human G-protein coupled receptor type protein.

Anti-HIV, cytostatic; antidiabetic; antiasmatic; antiinflammatory; haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic; antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR; cardian; dermatological; antifertility; hepatotropic; antiallergic; antipsoriatic; ophthalmological; antiangular; antihypoid; anticonvulsant; antineumatic; antiarthritic; G-protein coupled receptor; subfamily I; 93870 receptor; immune; inflammatory disorder; platelet disorder; skeletal; bone metabolism disorder; bone marrow mononuclear disorder; cellular proliferative; differentiative disorder; hormonal disorder; neurolgical disorder; cardiovascular disorder; viral disease; pain; liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial; hypochyroidism; hyperthyroidism; reproductive; fertility disorder; HIV; viral meningitis; fungal meningencephalitis; multiple sclerosis; Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia; Huntington's disease; heart failure; angina pectoris; dermatitis; myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease; inflammatory bowel disease; asthma; graft-versus-host disease; allergy; conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy; transgenic animal; human; gene; de.

Homo sapiens.

Key CDS

Location/Qualifiers

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MO200270657-A2.

12-SEP-2002.

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AC AAL53414;

DT 12-DEC-2002 (first entry)

DE 939 nt coding DNA of a human G-protein coupled receptor type protein.

XX Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
XX antibacterial; virucide; fungicide; analgesic; antiparamecan; GPCR;
XX cardiac; dermatological; antifertility; hepatotropic; anticallergic;
XX antiparasitic; ophthalmological; antianimal; anticonvulsant;
XX antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;
XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
XX cellular proliferative; differentiative disorder; hormonal disorder;
XX neurological disorder; cardiovascular disorder; viral disease; pain;
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
XX viral meningitis; fungal meningoencephalitis; multiple sclerosis;
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
XX Huntington's disease; heart failure; angina pectoris; dermatitis;
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
XX transgenic animal; human; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

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FT /tag= a

FT /partial

FT /product= "human G-protein coupled receptor type protein

PD 12-SEP-2002.

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PP	28-FEB-2002; 2002MO-US006455.
PR	01-MAR-2001; 2001US-0272677P.
PA	(MILL-) MILLENNIUM PHARM INC.
PI	Glucksmann MA;
XX	WPI: 2002-732793/79.
DR	P-PSDB; AAO22919.
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PT	New G-protein coupled receptor used in receptor assays as a target for
PT	diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT	inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT	disorders.
XX	
PS	Claim 5; Page 99-100; 105sp; English.
XX	
CC	The invention relates to an isolated polypeptide, which is a G-protein
CC	coupled receptor (GPCR) related to Subfamily I of G-protein coupled
CC	receptor type proteins (GPCRs), designated the 93870 receptor. The
CC	polypeptides, nucleic acid molecules and antibodies of the invention are
CC	useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC	monitoring clinical trials or pharmacogenetics), or in methods of
CC	treatment (e.g. therapeutic and prophylactic). They are useful in
CC	treating and diagnosing conditions related to aberrant activity or
CC	expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC	inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC	disorders, or bone marrow mononuclear disorders, as well as cellular
CC	proliferative and/or differentiative disorders, hormonal disorders,
CC	neurological disorders, cardiovascular disorders, viral diseases, liver
CC	diseases, and pain and metabolic disorders. Conditions that can be
CC	treated include cancer, diabetes mellitus, hypothyroidism,
CC	hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC	viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC	Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC	Huntington's disease, heart failure, angina pectoris, myocardial
CC	infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC	inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC	disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC	transgenic animals are useful for studying the function and/or activity
CC	of a 93870 protein and for identifying and/or evaluating modulators of
CC	93870 activities. The polynucleotides of the invention can be used in
CC	gene therapy. This polynucleotide sequence represents the cDNA of the
CC	1684 nucleotide human G-protein coupled receptor type protein of the
CC	invention
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Human GCREC-4 cDNA INCYTE ID 90012430CD1 SEQ ID 52.			
XX			
GCREC, Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative; cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide; protozoicide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;			

KM Parkinson's disease; Crohn's disease; constipation; infection;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200263004-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002W0-US003635.
XX
PR 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AR, Malia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Yang Y, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L,
XX
XX WPI; 2002-627557/67.
XX P-PSDB; AAB71325.
XX
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
XX treating a disease or condition associated with decreased expression or
XX over expression of functional GCREC e.g. cancer, Alzheimer's and
XX Parkinson's.
XX
XX Claim 113; Page 212-213; 239pp; English.
XX
XX This invention describes novel polypeptides which have anti-HIV,
XX antiarteriosclerotic, cytosolic, neuroprotective, antiinflammatory, virocidic,
XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virocidic,
XX antibacterial, fungicide and protozoacide activity. The products of the
XX invention are useful for treating a disease or condition associated with
XX decreased expression or over expression of functional G-protein coupled
XX receptors (GCREC), while antibodies generated against the polypeptide of
XX the invention are useful for diagnosing a condition or disease associated
XX with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
XX The compounds described in the invention can be used for gene therapy.
XX AAF8580-AAF8627 encode the GCREC proteins represented by AAB71322-
XX AAB71369, described in the disclosure of the invention
XX
SQ Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;
Query Match 99.8%; Score 937.4; DB 6; Length 1336;
Best Local Similarity 99.9%; Pred. No. 1.7e-267;
Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCAAAAATGACTCTCCCAAGTAGCTGCGCAATATCTCCAGAAATTCCTTTGG 60
DB 195 ATGCAAAAATGACTCTCCCAAGTAGCTGCGCAATATCTCCAGAAATTCCTTTGG 254
QY 61 GATCCTATAGTGAACCCCACTTAATGAGCTCTACTCTAGTGAATGAGGCGGCG 120
DB 255 GATCCTATAGTGAACCCCACTTAATGAGCTCTACTCTAGTGAATGAGGCGGCG 314
QY 121 GTGGGTGTCATTTTCATTTCTTCTCTGCTGTAATAATGAACCCGCTGACGACACC 180
DB 315 GTGGGTGTCATTTTCATTTCTTCTCTGCTGTAATAATGAACCCGCTGACGACACC 374
QY 181 ATGGCGGTCACTTAATGAGTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTCCG 240
DB 375 ATGGCGGTCACTTAATGAGTGTGTGTGTCACAGCGTTTCTGCTGACAGTGCATTTCCG 434

QY 241 TTGACCTACCTCATCAAGAGAATTGGANTTTGGGCTGCCCTTCTGCAAAATTTGGAGT 300
DB 435 TTGACCTACCTCATCAAGAGAATTGGANTTTGGGCTGCCCTTCTGCAAAATTTGGAGT 494
QY 301 GCCATGCTGACATCCACATGATGACTCAAGTCTTAATCTATGTGTGATCTGCTGAC 360
DB 495 GCCATGCTGACATCCACATGATGACTCAAGTCTTAATCTATGTGTGATCTGCTGAC 554
QY 361 AGATACCTATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTTACAGAAATCTGATGCT 420
DB 555 AGATACCTATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTTACAGAAATCTGATGCT 614
QY 421 GTGGGTGACAGTGTGTCATGTGGAACGCTGAGTGTGATGATGATGATGATGATGATG 480
DB 615 GTGGGTGACAGTGTGTCATGTGGAACGCTGAGTGTGATGATGATGATGATGATGATG 674
QY 481 TCCCGGTATGAAATCCATGAGGAATACATGAGAGCACTGTTTAAATTTTCAAAAGAG 540
DB 675 TCCCGGTATGAAATCCATGAGGAATACATGAGAGCACTGTTTAAATTTTCAAAAGAG 734
QY 541 CTGGCTTACATATGATGAAAAATCATCACTATATGATATGATATTTTGTCTACCGCT 600
DB 735 CTGGCTTACATATGATGAAAAATCATCACTATATGATATGATATTTTGTCTACCGCT 794
QY 601 GCTGTGATCTGTGTGCTTCCAGGCTTCAATCATTTATGATGATGATGATGATGATGATG 660
DB 795 GCTGTGATCTGTGTGCTTCCAGGCTTCAATCATTTATGATGATGATGATGATGATGATG 854
QY 661 CACTCTTATCATCCACAGAGATCTGAGGCTCAGCTGAAAAACCTATTTTATAGAG 720
DB 855 CACTCTTATCATCCACAGAGATCTGAGGCTCAGCTGAAAAACCTATTTTATAGAG 914
QY 721 GTCATCTGTGTTGTTTCTTCTTCCATCAGATGTTTAGATCTATTTAGTGAATGTG 780
DB 915 GTCATCTGTGTTGTTTCTTCTTCCATCAGATGTTTAGATCTATTTAGTGAATGTG 974
QY 781 ACGCATTCGAATGCGCTGATGAGCAAGGTTGATTTTAAACGAATCTTCTGAGTGA 840
DB 975 ACGCATTCGAATGCGCTGATGAGCAAGGTTGATTTTAAACGAATCTTCTGAGTGA 1034
QY 841 ACGCAATTAATGCTGATGATGATTTGCTTCTTCTTCTTGGGGAAGCCATTTAG 900
DB 1035 ACGCAATTAATGCTGATGATGATTTGCTTCTTCTTCTTGGGGAAGCCATTTAG 1094
QY 901 CAAAAGTAAATGCTTATGAAATGTTGTTTGTGCCGT 939
DB 1095 CAAAAGTAAATGCTTATGAAATGTTGTTTGTGCCGT 1133
RESULT 4
AAF8584
ID AAF8584 standard; cDNA; 1340 BP.
XX
XX AAF8584;
XX
XX 19-NOV-2002 (first entry)
XX
DE Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.
XX
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytosolic; neuroprotective; antiinflammatory; hepatotropic; laxative;
XX cerebroprotective; antiinflammatory; virocidic; antibacterial; fungicide;
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection;
XX gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX W0200263004-A2.
XX
XX 15-AUG-2002.
XX

PF 06-FEB-2002; 2002WO-US003635.
XX
PR 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallik DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Rankumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;
PI Graul RC, Khan PA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX
DR WPI; 2002-627557/67.
XX P-PSDB; AAB71326.
XX
PT New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX
PS Claim 114; Page 213; 239p; English.
XX
XX This invention describes novel polypeptides which have anti-HIV,
XX antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virocidic,
XX antibacterial, fungicidal and protozoacidal activity. The products of the
XX invention are useful for treating a disease or condition associated with
XX decreased expression or over expression of functional G-protein coupled
XX receptors (GCREC), while antibodies generated against the polypeptide of
XX the invention are useful for diagnosing a condition or disease associated
XX with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
XX The compounds described in the invention can be used for gene therapy.
XX AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-
XX AAB71369, described in the disclosure of the invention
SQ
Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;
Query Match 98.8%; Score 928.2; DB 6; Length 1340;
Best Local Similarity 99.7%; Pred. No. 9,4e-265;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 AATATGACCTTCCCAAGTATGCTGACCAATATCTCCAGAAATCTCTTGATCCT 66
DB 205 ACAGGTGACTTCCCAAGTATGCTGACCAATATCTCCAGAAATCTCTTGATCCT 264
QY ATATGACACCCCACTTATCAGCTCTACTTCAATAGTGTATTTGGCGGGCTGGGGCT 126
DB 265 ATATGACACCCCACTTATCAGCTCTACTTCAATAGTGTATTTGGCGGGCTGGGGCT 324
QY 127 GTCATTTCAATTTCTTCTCTCTGCTGTAATAATGAAACCCGCTCATGTAACCAACATGCG 186
DB 325 GTCATTTCAATTTCTTCTCTCTGCTGTAATAATGAAACCCGCTCATGTAACCAACATGCG 384
QY 187 GTCATTTCAATTTCTTCTCTCTGCTGTAATAATGAAACCCGCTCATGTAACCAACATGCG 246
DB 385 GTCATTTCAATTTCTTCTCTCTGCTGTAATAATGAAACCCGCTCATGTAACCAACATGCG 444
QY 247 TACCTATCAAGAAGACTTGATGTTGGCTGCGCTTCGCAAAATTTGGAGTGCATG 306
DB 445 TACCTATCAAGAAGACTTGATGTTGGCTGCGCTTCGCAAAATTTGGAGTGCATG 504
QY 307 CTGCAATCCAGATGTAACCTCAAGCTTCTATTTATGTGTGATTCCTGTGACCAAGATAC 366
DB 505 CTGCAATCCAGATGTAACCTCAAGCTTCTATTTATGTGTGATTCCTGTGACCAAGATAC 564

QY 367 CTGATCTCTTCAAGTGCAGAAAGCAAAAGTGAATTCCTACAGAAAACCTGATGCTG 426
DB 565 CTGATCTCTTCAAGTGCAGAAAGCAAAAGTGAATTCCTACAGAAAACCTGATGCTG 624
QY 427 GCCAGTCTGGCATGTGAGACGCTGTGATGTCATTTGGTATCCCTGTTGTCCTCCGG 486
DB 625 GCCAGTCTGGCATGTGAGACGCTGTGATGTCATTTGGTATCCCTGTTGTCCTCCGG 684
QY 487 TATGAAATCCATAGGAATACAAATGAGAGACACTGTTTTAAATTCACAAAGACTTGT 546
DB 685 TATGAAATCCATAGGAATACAAATGAGAGACACTGTTTTAAATTCACAAAGACTTGT 744
QY 547 TACACATATGTGAAATTCATCATATATGATATGTCATTTTGTCTATAGCCGTGCTG 606
DB 745 TACACATATGTGAAATTCATCATATATGATATGTCATTTTGTCTATAGCCGTGCTG 804
QY 607 ATTCTGTGGTCTTCCAGGCTTCATCATATATGATATGTCATTTTGTCTATAGCCGTG 666
DB 805 ATTCTGTGGTCTTCCAGGCTTCATCATATATGATATGTCATTTTGTCTATAGCCGTG 864
QY 667 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGTCTATC 726
DB 865 TTACTATCCACAGAGAGTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGTCTATC 924
QY 727 CTGTGTTGTTCTTCTTCCCTACAGTCTTTAGATCTATTTACTTGAATGTTGACGCAT 786
DB 925 CTGTGTTGTTCTTCTTCCCTACAGTCTTTAGATCTATTTACTTGAATGTTGACGCAT 984
QY 787 TCCATATCCCTGAGAGAGTTCGATTTTATACGAATCTCTTGAAGTGAACGCA 846
DB 985 TCCATATCCCTGAGAGAGTTCGATTTTATACGAATCTCTTGAAGTGAACGCA 1044
QY 847 ATTAGTGTATGATATTTGCTTCTTGTCTTTGGGGAAGCCATGTTTAAAGCAAAAG 906
DB 1045 ATTAGTGTATGATATTTGCTTCTTGTCTTTGGGGAAGCCATGTTTAAAGCAAAAG 1104
QY 907 ATTAATGCTTATGAAATGTTGTTTGTGCGCT 939
DB 1105 ATTAATGCTTATGAAATGTTGTTTGTGCGCT 1137
RESULT 5
AAF88585
ID AAF88585 standard; cDNA; 1460 BP.
XX
XX AAF88585;
XX
XX 19-NOV-2002 (first entry)
XX
XX Human GCREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.
XX
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
XX cerebroprotective; antiinflammatory; virocidic; antibacterial; fungicide;
XX protozoacidal; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection;
XX gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200263004-A2.
XX
XX 15-AUG-2002.
XX
XX
XX
XX 06-FEB-2002; 2002WO-US003635.
XX
XX
XX 07-FEB-2001; 2001US-0267322P.
XX 23-FEB-2001; 2001US-0271215P.
XX 08-MAR-2001; 2001US-0274551P.
XX 23-MAR-2001; 2001US-0278507P.
XX 30-MAR-2001; 2001US-0280597P.
XX 02-APR-2001; 2001US-0281107P.
XX 06-APR-2001; 2001US-0282121P.

XX (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG, Hefalia AJA,
PI Kalliock DA, Gandhi AR, Walla NK, Arvizu C, Ellitford VS, Bulford N, Lu DAM,
PI Ramkumar J, Pel J, Tang Y, Yue R, Reddy R, Bulford N, Lu DAM,
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA,
PI Warren BA, Yang J, Lee EA, Harland L,
XX
DR WPI, 2002-627557/67.
DR P-PSDS; AAB71327.
XX
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
PS
PS Claim 115; Page 213-214; 239pp; English.
XX
XX This invention describes novel polypeptides which have anti-HIV,
CC antiarteriosclerotic, cyostatic, neuroprotective, antiparkinsonian,
CC heparinocleptive, laxative, cerebroprotective, antiinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or over expression of functional G-protein coupled
CC receptors (GCREC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-
CC AAB71369, described in the disclosure of the invention
SQ
SQ Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;
Query Match 98.8%; Score 928.2; DB 6; Length 1460;
Best Local Similarity 99.7%; Pred. No. 9.8e-265;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 AATGTGACTTCCCAAGTATGCTGGCCACAAATCTCCAGAAATCTCTTGCGATCCT 66
DB 325 ACAGGTACTTCCCAAGTATGCTGGCCACAAATCTCCAGAAATCTCTTGCGATCCT 384
QY 67 ATAGTGACCCCACTTAATGAGCTCTTACTTCAATGCTTATGCGGGCGCTGCGGCT 126
DB 385 ATAGTGACCCCACTTAATGAGCTCTTACTTCAATGCTTATGCGGGCGCTGCGGCT 444
QY 127 GTCATTTCCATTTCTTCTCTGCTGGTGAATAATGAACACCGGTCAAGTACCAACATGCG 186
DB 445 GTCATTTCCATTTCTTCTCTGCTGGTGAATAATGAACACCGGTCAAGTACCAACATGCG 544
QY 187 GTCATTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
DB 505 GTCATTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
QY 247 TACCTCATCAAGAAGACTTGGATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
DB 565 TACCTCATCAAGAAGACTTGGATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 307 CTGACATCCACATGTAATCTCACTCTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
DB 625 CTGACATCCACATGTAATCTCACTCTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
QY 367 CTGATCTTCTTCAAGTCAAGAACAAAGTGAATTTCAAGAAATCTGATGCTGCTGCT 426
DB 685 CTGATCTTCTTCAAGTCAAGAACAAAGTGAATTTCAAGAAATCTGATGCTGCTGCT 744
QY 427 GCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
DB 745 GCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
QY 487 TATGATTCATGATGAGTAATCAATGAGGAGACTGTTTAAATTTCAAAAGACTTGTCT 546

DB 805 TATGATTCATGATGAGTAATCAATGAGGAGACTGTTTAAATTTCAAAAGACTTGTCT 864
QY 547 TACACATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGATG 606
DB 865 TACACATATGTAATAATCATCAATATGATGATGATGATGATGATGATGATGATGATG 924
QY 607 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
DB 925 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
QY 667 TTACTATCCACACAGAGAGTCTGGGCTGAGCTGAAACCTATTTTATAGGGTCACT 726
DB 985 TTACTATCCACACAGAGAGTCTGGGCTGAGCTGAAACCTATTTTATAGGGTCACT 1044
QY 727 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
DB 1045 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
QY 787 TCCAAATGCTGATGAGCAAGGTTGCAATTTTATAGAAATCTCTGAGTGAACAGA 846
DB 1105 TCCAAATGCTGATGAGCAAGGTTGCAATTTTATAGAAATCTCTGAGTGAACAGA 1164
QY 847 ATTAGCTGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
DB 1165 ATTAGCTGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
QY 907 ATTAGCTGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
DB 1225 ATTAGCTGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
RESULT 6
AAH51009
ID AAH51009 standard; DNA; 2525 BP.
XX
XX AAH51009;
XX
XX 28-AUG-2001 (first entry)
XX
XX Human nGPER16 coding sequence #2.
XX
XX G protein-coupled receptor; nGPER; seven transmembrane receptor;
KM signal transduction; schizophrenia; thyroid disorder; renal failure;
KM rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KM cardiovascular disease; proliferative disorder; hormonal disorder;
KM neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KM attention deficit-hyperactivity disorder; attention deficit disorder;
KM Parkinson's disease; migraine; senile dementia; inflammatory disease;
KM rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KM neuroprotective; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200136473-A2.
XX
XX PD 25-MAY-2001.
XX
XX PF 16-NOV-2000; 2000MO-US031581.
XX
XX 16-NOV-1999; 99US-0165838P.
PR 17-NOV-1999; 99US-0166071P.
PR 19-NOV-1999; 99US-0166678P.
PR 28-DEC-1999; 99US-0173396P.
PR 22-FEB-2000; 2000US-0184129P.
PR 28-FEB-2000; 2000US-0185421P.
PR 28-FEB-2000; 2000US-0185544P.
PR 02-MAR-2000; 2000US-0186530P.
PR 03-MAR-2000; 2000US-0186811P.
PR 09-MAR-2000; 2000US-0188114P.
PR 17-MAR-2000; 2000US-0190310P.
PR 21-MAR-2000; 2000US-0190800P.
PR 20-APR-2000; 2000US-0198568P.

PT New nucleic acids and polypeptides of the ng protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.

XX Example 1; Page 84-85; 244pp; English.

XX The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an ngPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder
CC and for identifying a compound useful as a modulator of binding between
CC ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in AB570202-AB570248, AB570318 and AB570243 are the DNAs
CC encoding the ngPCRs (also referred to as beGPCRs)

XX Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

Query Match 98.8%; Score 928.2; DB 6; Length 2525;
Best Local Similarity 99.7%; Pred. No. 1.3e-264;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AATATGACTTCCCAAGTATGCTGGGCAACAATCCCGAGAAATCTCTTGCATTCCT 66
DB 9 ACGGTGACTTCCCAAGTATGCTGGGCAACAATCCCGAGAAATCTCTTGCATTCCT 68
QY 67 ATAGTACACCCCACTTAATCAGCTCTACTATAGTGTCTTATGCGGGGCTGTGGGT 126
DB 69 ATAGTACACCCCACTTAATCAGCTCTACTATAGTGTCTTATGCGGGGCTGTGGGT 128
QY 127 GTATTTCCATTTTCTCTCTGTGGAATAAGAACCCGGTCACTGACACCATGGGG 186
DB 129 GTATTTCCATTTTCTCTCTGTGGAATAAGAACCCGGTCACTGACACCATGGGG 188
QY 187 GTCAATTAATCTGGTGGTGTGCAAGAGTTTTCTGTGTCAGTGCATTTGCTTGACC 246
DB 189 GTCAATTAATCTGGTGGTGTGCAAGAGTTTTCTGTGTCAGTGCATTTGCTTGACC 248
QY 247 TACCTCATCAAGAAGACTTGATGTTGGGCTGCCCTTGCAAATTTGTAGTGCATG 306
DB 249 TACCTCATCAAGAAGACTTGATGTTGGGCTGCCCTTGCAAATTTGTAGTGCATG 308
QY 307 CTGCAATCCACATGTAACCTCAAGTTCCTTATGATGTGATTCCTGGTCAACAATAC 366
DB 309 CTGCAATCCACATGTAACCTCAAGTTCCTTATGATGTGATTCCTGGTCAACAATAC 368
QY 367 CTGATCTTCTTCAAGTGCAAAGAACAAGTGAATTCACAGAAATCGCATGCTGGGCT 426
DB 369 CTGATCTTCTTCAAGTGCAAAGAACAAGTGAATTCACAGAAATCGCATGCTGGGCT 428
QY 427 GCCAGTCTGGCATGTGAGCGCTGTGATTTGCTATGCTGATCCCTGTGTTCTCCCG 486
DB 429 GCCAGTCTGGCATGTGAGCGCTGTGATTTGCTATGCTGATCCCTGTGTTCTCCCG 488
QY 487 TATGGAATCCATGAGGAATTCATATGAGAGCACTGTTTAAATTTCACAAAAGCTTGCT 546
DB 489 TATGGAATCCATGAGGAATTCATATGAGAGCACTGTTTAAATTTCACAAAAGCTTGCT 548

QY 547 TACACATATGTAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTTGCTG 606
DB 549 TACACATATGTAATAATCATCACTATATGATGATCATTTTGTGATAGCCGTTGCTG 608
QY 607 ATTCTGTGGTCTTCAGGTCTTCATCATATATGATGTGAGAGCAAGCTACGCACTCT 666
DB 609 ATTCTGTGGTCTTCAGGTCTTCATCATATATGATGTGAGAGCAAGCTACGCACTCT 668
QY 667 TTACATATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCAATC 726
DB 669 TTACATATCCACAGAGAGTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCAATC 728
QY 727 CTGTGTTGTTCTTCCCTACAGTCTCTTAGATCTATTAATGATTTGACGCAAT 786
DB 729 CTGTGTTGTTCTTCCCTACAGTCTCTTAGATCTATTAATGATTTGACGCAAT 788
QY 787 TCCAAATGCTGTAGACAGCAAGGTTCATTTTAAAGAAATCTTTGATGTAAACAGCA 846
DB 789 TCCAAATGCTGTAGACAGCAAGGTTCATTTTAAAGAAATCTTTGATGTAAACAGCA 848
QY 847 ATTAGCTGTATGATTTGCTCTTGTCTTTGGGGAAAGCATTTGTTAAGCAAAAG 906
DB 849 ATTAGCTGTATGATTTGCTCTTGTCTTTGGGGAAAGCATTTGTTAAGCAAAAG 908
QY 907 ATAAATGGCTATGGAATTTGTTTGGGCCGT 939
DB 909 ATAAATGGCTATGGAATTTGTTTGGGCCGT 941

RESULT 8
ADC86554
ID ADC86554 standard; DNA; 113306 BP.

XX AC ADC86554;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR gene SEQ ID NO:1007.

XX KW ds; gene; human; GPCR;

XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX DR WPI; 2003-315783/31.

XX DR P-PSDB; ADC86555.

PT New polynucleotide, useful for preparing a composition for treating a

PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 1007; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The

CC polynucleotide sequences shown in AD085548-AD087616 encode GPCR's of the
CC invention.
XX
SQ Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
Query Match 98.8%; Score 927.8; DB 10; Length 113306;
Best Local Similarity 99.8%; Pred. No. 1.3e-263;
Matches 929; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 ATGTGACCTTCCCAAGTATGCTGGCCCAATACCTCCAGGAATTCCTTGGCATCTAT 68
DB 11524 AGGGACCTTCCCAAGTATGCTGGCCCAATACCTCCAGGAATTCCTTGGCATCTAT 11583
QY 69 AGTGAACCCCACTTATACAGCCCTTACTCATAGTCTTATGGCGGGCTGGGGGCTG 128
DB 11584 AGTGAACCCCACTTATACAGCCCTTACTCATAGTCTTATGGCGGGCTGGGGGCTG 11643
QY 129 CATTTCCATTCTTCTCTCTGTGTAATAACACCCGGTCAGTGACCAACATGGCGGT 188
DB 11644 CATTTCCATTCTTCTCTCTGTGTAATAACACCCGGTCAGTGACCAACATGGCGGT 11703
QY 189 CATTAACTTGGTGTGTCCACAGCGTTTTCGTGTCAGAGTCCATTTCCTTGAACCTA 248
DB 11704 CATTAACTTGGTGTGTCCACAGCGTTTTCGTGTCAGAGTCCATTTCCTTGAACCTA 11763
QY 249 CCTCATCAAGAAAGCTTGGAGTGTGGGCTGCCCTTTCGAAATTTGTGATGCCATGCT 308
DB 11764 CCTCATCAAGAAAGCTTGGAGTGTGGGCTGCCCTTTCGAAATTTGTGATGCCATGCT 11823
QY 309 GCACATCCACATGATGATCTCAAGTTCCTATTCATAGTGTGTATCTGGTGCACAGATACCT 368
DB 11824 GCACATCCACATGATGATCTCAAGTTCCTATTCATAGTGTGTATCTGGTGCACAGATACCT 11883
QY 369 CATCTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAACTGCATGCTGGCTGC 428
DB 11884 CATCTCTTCAAGTGCAGAAAGCAAAAGTGAATTTCTACAGAAACTGCATGCTGGCTGC 11943
QY 429 CAGTGTGGAGATGTGACCGTGTGTATGTCATTTGTGTATGTCATGCTGGTGTCTCCGGTA 488
DB 11944 CAGTGTGGAGATGTGACCGTGTGTATGTCATTTGTGTATGTCATGCTGGTGTCTCCGGTA 12003
QY 489 TGGATTCATGAGGAATATACATGAGAGACACTGTTTAAATTTCAACAAAGAGCTGTGTA 548
DB 12004 TGGATTCATGAGGAATATACATGAGAGACACTGTTTAAATTTCAACAAAGAGCTGTGTA 12063
QY 549 CACATATGTGAAAATCATCACTATATGATGATCATTTTGTCTATAGCCGTTGCTGTGAT 608
DB 12064 CACATATGTGAAAATCATCACTATATGATGATCATTTTGTCTATAGCCGTTGCTGTGAT 12123
QY 609 TCTGTGTGCTTTCAGAGTCTTCACTATATGATGATGTCAGAGAGCTACGCCATCTTT 668
DB 12124 TCTGTGTGCTTTCAGAGTCTTCACTATATGATGATGTCAGAGAGCTACGCCATCTTT 12183
QY 669 ACTATCCACACAGAGGTTCTGGGCTGACGTGAAAACCTATTTTATAGGGGTCAATCCT 728
DB 12184 ACTATCCACACAGAGGTTCTGGGCTGACGTGAAAACCTATTTTATAGGGGTCAATCCT 12243
QY 729 TGTGTGTGCTTTCCTTACAGTTCCTTATAGATCTATATCTGATATGTTGTGACGATTC 788
DB 12244 TGTGTGTGCTTTCCTTACAGTTCCTTATAGATCTATATCTGATATGTTGTGACGATTC 12303
QY 789 CAATGCTGTAGACAGAGGTCATTTTAAAGAAATCTTGTGATGTAACAGCAAT 848
DB 12304 CAATGCTGTAGACAGAGGTCATTTTAAAGAAATCTTGTGATGTAACAGCAAT 12363
QY 849 TACGTGTATGATTTGCTCTTGTCTTGTGGGGAGACATGTTTAAAGAAAGAT 908
DB 12364 TACGTGTATGATTTGCTCTTGTCTTGTGGGGAGACATGTTTAAAGAAAGAT 12423
QY 909 AATTGCTTATGAAATGTGTTTGTGCGCT 939
DB 12424 AATTGCTTATGAAATGTGTTTGTGCGCT 12454

RESULT 9
ID ABK87351 standard; cDNA; 1051 BP.
XX
AC ABK87351;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human cDNA encoding G protein-coupled receptor IGS70.
XX
KW Human; sex; gene; G protein-coupled receptor; GPCR; IGS70; CNS;
XX psychiatric disorder; central nervous system disorder; schizophrenia;
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
KW heart failure; angina pectoris; myocardial infarction; kidney disease;
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
KW osteoporosis; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 60..977
FT /tag= a
FT /product= "GPCR IGS70"
XX
PN MO200244212-A2.
XX
PD 06-JUN-2002.
XX
PF 23-NOV-2001; 2001MO-EP013706.
XX
PR 30-NOV-2000; 2000BP-00204280.
XX P-DEC-2000; 2000US-0251045P.
XX (SOLV) SOLVAY PHARM BV.
XX
XX Deleersnijder W, Blockx H, De Moor L;
XX WPI; 2002-527703/56.
XX P-PSDB; AAU99179.
XX
PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating
PT dysfunction, disorders or disease related to lung, bone marrow, spinal
PT cord immune system.
XX
XX
PS Claim 1; Page 6; 58pp; English.
XX
XX The invention relates to a G protein-coupled receptor (GPCR) IGS70
XX polypeptide including sequences that are 98-99.6% identical. Also
XX included are the polynucleotide encoding IGS70 (including sequences 98-
XX 99.6% identical to the polynucleotide or the DNA insert contained in
XX plasmid CBS 109818), a hybridisation probe derived from the
XX polynucleotide, a DNA or RNA expression system producing IGS70, a host
XX comprising the expression system, IGS70 receptor membrane preparation
XX derived from the cell, an antibody immunospecific for IGS70, IGS70 is
XX useful for diagnosing a disease or a susceptibility to disease in a
XX subject related to expression or activity of the IGS70 polypeptide in a
XX subject by determining the presence or absence of mutation in the
XX nucleotide sequence encoding IGS70 in the genome of the subject in a
XX sample derived from the subject. IGS70 is also useful identifying agonist
XX or antagonist. The IGS70 protein, polynucleotide, antibody and identified
XX ant/agonists are useful for treating psychiatric and central nervous
XX system (CNS) disorders such as schizophrenia, Alzheimer's disease,
XX multiple sclerosis, anxiety, cardiovascular diseases such as heart
XX failure, angina pectoris, myocardial infarction, kidney disease such as
XX renal failure, gastrointestinal disorders such as irritable bowel
XX syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
XX inflammation, cancer, asthma, infection (such as bacterial, viral,
XX fungal, protozoal) especially human immunodeficiency virus infection
XX (HIV), diabetes, osteoporosis and allergies. The present sequence encodes
XX the human GPCR IGS70

XX Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 98.6%; Score 926.2; DB 6; Length 1051;
Best Local Similarity 99.7%; Pred. No. 3.2e-264;
Matches 928; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 9 ATGTGACCTTCCCAAGATATGCTGGCCACATATACCTCCAGAAATTCCTTTGGATCCTTAT 68
DB 44 AGGTGACCTTCCCAAGATATGCTGGCCACATATACCTCCAGAAATTCCTTTGGATCCTTAT 103
QY 69 AGTGAACCCCACTTATATGAGCTTCTATATGCTTATATGAGGCGGTGGTGGTGT 128
DB 104 AGTGAACCCCACTTATATGAGCTTCTATATGAGCTTATGAGGCGGTGGTGGTGT 163
QY 129 CATTTTCATTTCTTTCTCTCTGTTGTAATAATGAACCCCGGTGCTGATGACCATGCGGT 188
DB 164 CATTTTCATTTCTTTCTCTCTGTTGTAATAATGAACCCCGGTGCTGATGACCATGCGGT 223
QY 189 CATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 248
DB 224 CATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 283
QY 249 CCTCATCAAGAAAGACTTGAATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCTGCT 308
DB 284 CCTCATCAAGAAAGACTTGAATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCTGCT 343
QY 309 GCACATCCACATGATACCTCAGCTTCTATTTCTATGTTGATGCTGCTGCTGCTGCTGCT 368
DB 344 GCACATCCACATGATACCTCAGCTTCTATTTCTATGTTGATGCTGCTGCTGCTGCTGCT 403
QY 369 CATCTCTTCAAGTGCAGAAAGACAAAGTGAATCTTACAGAAACTGCATGCTGGGCTG 428
DB 404 CATCTCTTCAAGTGCAGAAAGACAAAGTGAATCTTACAGAAACTGCATGCTGGGCTG 463
QY 429 CAGTGTGCGCATGTGACGCTGTGATGTCATTTGTGTAACCCCTGTTCTCTCCGGTA 488
DB 464 CAGTGTGCGCATGTGACGCTGTGATGTCATTTGTGTAACCCCTGTTCTCTCCGGTA 523
QY 489 TGGAAATCCATGAGAAATACAAATGAGAGCAGCTGTTTAAATTTCAAAAGAGCTTGT 548
DB 524 TGGAAATCCATGAGAAATACAAATGAGAGCAGCTGTTTAAATTTCAAAAGAGCTTGT 583
QY 549 CACATATGTAATAATCATCAACTATATATGATGATCATTTTGTGATGCGGTGCTGAT 608
DB 584 CACATATGTAATAATCATCAACTATATATGATGATCATTTTGTGATGCGGTGCTGAT 643
QY 609 TCTGTGTCTTCCAGGCTTTCATCATTTATGTTGATGTTGAGAGCTACGCCACTT 668
DB 644 TCTGTGTCTTCCAGGCTTTCATCATTTATGTTGATGTTGAGAGCTACGCCACTT 703
QY 669 ACTATCCCAACAGAGGTTCTGGGCTCAGCTGAAAAAATTTTATATAGGGGTCACTCT 728
DB 704 ACTATCCCAACAGAGGTTCTGGGCTCAGCTGAAAAAATTTTATATAGGGGTCACTCT 763
QY 729 TGTGTGTCTTCCCTACAGGTTCTTTAGATCTTATCTTATGATGTTGAGAGCTT 788
DB 764 TGTGTGTCTTCCCTACAGGTTCTTTAGATCTTATCTTATGATGTTGAGAGCTT 823
QY 789 CAATGCTGTAGAGAGAGGTTGATTTTAAAGAAATCTTCTGATGTTAAACAGCAAT 848
DB 824 CAATGCTGTAGAGAGAGGTTGATTTTAAAGAAATCTTCTGATGTTAAACAGCAAT 883
QY 849 TACGTCTATGATTTGTTCTTTGCTTTTGGGGAGAGCATTTGTTTAAAGAAAGAT 908
DB 884 TACGTCTATGATTTGTTCTTTGCTTTTGGGGAGAGCATTTGTTTAAAGAAAGAT 943
QY 909 AATTGGCTATGAAATTTGTTTGGCGGT 939
DB 944 AATTGGCTATGAAATTTGTTTGGCGGT 974
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RESULT 10

```
AAI44713
ID AAI44713 standard; DNA; 918 BP.
XX AC AAI44713;
XX DT 03-MAY-2002 (first entry)
XX DE Human testis originated G-protein coupled receptor TGR10 coding sequence.
XX KW Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
XX KW cytosolic; immunomodulator; cardiatic; neuroprotective; gene therapy;
XX KW inflammation; nervous system disease; circulatory system disease; cancer;
XX KW metabolic disease; immunological disease; gastrointestinal disease; gene;
XX ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..918
XX FT /tag= a
XX FT /product= "TGR10"
XX PN WO200196567-A1.
XX PD 20-DEC-2001.
XX PF 14-JUN-2001; 2001WO-0P005061.
XX PR 15-JUN-2000; 2000JP-00184596.
XX PR 19-JUL-2000; 2000JP-00223887.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Moriya T, Ito T, Shintani Y, Miyajima N;
XX DR WPI; 2002-098071/13.
XX DR P-PSDB; AAM483989.
XX PT Human testis-originated G protein-coupled receptor protein TGR10 and
XX PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.
XX PT diseases of central nervous system, inflammations and diseases of
XX PT circulatory system.
XX PS Claim 5; Page 99; 110pp; Japanese.
XX CC The present invention provides the protein and coding sequences of a
XX CC novel human testis-originated G protein-coupled receptor protein TGR10.
XX CC The sequences can be used in the development of drugs for the treatment
XX CC of diseases of the central nervous system, inflammations, diseases of the
XX CC circulatory system, cancer, metabolic diseases, immunological diseases,
XX CC and diseases of the gastrointestinal system. The present sequence is the
XX CC coding sequence of the invention
XX SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
XX Query Match 97.3%; Score 913.4; DB 6; Length 918;
XX Best Local Similarity 99.9%; Pred. No. 1.9e-260;
XX Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 ATGCTGGCCACAAATACCTCCAGAAATTCCTTGCATCTTAATGAGACACCCACTTA 84
DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTGCATCTTAATGAGACACCCACTTA 60
QY 85 ATCAGCCTTACTTCAATAGTGTATTTGCGGGGCTGTGGGTGTATTTCCATTTCTTTTC 144
DB 61 ATCAGCCTTACTTCAATAGTGTATTTGCGGGGCTGTGGGTGTATTTCCATTTCTTTTC 120
QY 145 CTCCTGGTGAATAATGAACCCGGTCAAGTGAACCAATGAGCGGCTATTAATCTGGTGGT 204
DB 121 CTCCTGGTGAATAATGAACCCGGTCAAGTGAACCAATGAGCGGCTATTAATCTGGTGGT 180
QY 205 GTCCACAGCGTTTTCTGTGACAGTGCATTTGCTTGACCTTACCTGATCAAGAGACT 264
```


XX	Novel endogenous and non-endogenous versions of G protein-coupled	
PT	receptor useful for identification of candidate compounds as receptor	
PT	agonists or antagonists for use as therapeutic agents.	
XX		
PS		
XX		
XX	Claim 7; Page 56-57; 84pp; English.	
CC	The present invention provides the protein and coding sequences of	
CC	several human G-protein coupled receptors (GPCRs). These can be used in	
CC	the identification of candidate compounds as receptor agonists or inverse	
CC	agonists having applicability as therapeutic agents. The present sequence	
CC	is a GPCR coding sequence of the invention	
XX		
XX		
Sequence	918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;	
Query Match	97.3%; Score 913.4; DB 6; Length 918;	
Best Local Similarity	99.9%; Pred. No. 1.9e-260;	
Matches	914; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
Qy	25 ATGCGTGGCAACAATACCTCCAGAAATTCCTTCGATCCTATATGTGACACCCCACTTA	84
Db	1 ATGCGTGGCAACAATACCTCCAGAAATTCCTTCGATCCTATATGTGACACCCCACTTA	60
Qy	85 ATCAGCCTCTACTTCAATATAGTGTCTTATTTGGCGGGCTGTGTGGTGTCAATTTTCATT	144
Db	61 ATCAGCCTCTACTTCAATATAGTGTCTTATTTGGCGGGCTGTGTGGTGTCAATTTTCATT	120
Qy	145 CTCCTGTGTGAAAATGAACACCGCGGTACAGTGAACACCATGGCGGTCACTTAATCTTG	204
Db	121 CTCCTGTGTGAAAATGAACACCGCGGTACAGTGAACACCATGGCGGTCACTTAATCTTG	180
Qy	205 GTCCACAGGCTTTTCTGTGTGACAGTGCATTCGCTTACCTCAATCAAGAAAGCT	264

QY	265	TTGGAGTTTGGGCTGCGCCCTTCGAAAATTGAGAGGCGAAGCTGACATCCAAATGAC	324
Db	241	TGGAGTTTGGGCTGCGCCCTTCGAAAATTGAGAGGCGAAGCTGACATCCAAATGAC	300
QY	325	CTCAGCTTCTATTTCTATGTGGTGAATCCTGGTCAACAATACCTCATCTTCTCAAGTC	384
Db	301	CTCAGCTTCTATTTCTATGTGGTGAATCCTGGTCAACAATACCTCATCTTCTCAAGTC	360
QY	385	AAAGCAAAAGTGAATTTCAAGAAAATGCAATGCTGTGGCTGCGAAGTCTGGCAATGG	444
Db	361	AAAGCAAAAGTGAATTTCAAGAAAATGCAATGCTGTGGCTGCGAAGTCTGGCAATGG	420
QY	445	ACGCTGGTGAATGTCAATGTGGTGAACCCCGTGTGTCTCCGGTATGGAATCCATGAGAA	504
Db	421	ACGCTGGTGAATGTCAATGTGGTGAACCCCGTGTGTCTCCGGTATGGAATCCATGAGAA	480
QY	505	TACAAATGAGAGCACTGTTTAAATTTCAAAAAGACTTGCTTACACATATGTGAAATC	564
Db	481	TACAAATGAGAGCACTGTTTAAATTTCAAAAAGACTTGCTTACACATATGTGAAATC	540
QY	565	ATCAACTATATATATGTCAATTTTGTGCATAGGCGATGCTGATCTGTGGCTTCCAG	624
Db	541	ATCAACTATATATATGTCAATTTTGTGCATAGGCGATGCTGATCTGTGGCTTCCAG	600
QY	625	GTCTTCATCATATATGTGATGAGTGAAGAGCTACAGCACTCTTATCTATCCCAACGAG	684
Db	601	GTCTTCATCATATATGTGATGAGTGAAGAGCTACAGCACTCTTATCTATCCCAACGAG	660
QY	685	TTCTGGGCTCAAGTGAATAAATCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC	744
Db	661	TTCTGGGCTCAAGTGAATAAATCTATTTTATAGGGGTCATCCTGTGTTGTTCTCTCC	720
QY	745	TACAGTTCTTAAAGATCATATCTAGTGAATGTGTGAGCATTTCCAAATGCTGTAGCAG	804
Db	721	TACAGTTCTTAAAGATCATATCTAGTGAATGTGTGAGCATTTCCAAATGCTGTAGCAG	780
QY	805	AAGGTGCAATTTTATPACAAAATCTTCTTGAAGTGTAPACAGAAATGACTGCTATGATTTG	864

Db 781 AAGTTGCAATTTTAAACGAAATCTTCTGAGTGTAACAGCAATTAGCTGATGATTTG 840
QY 865 CTCTCTTTTCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATATGCTTATGCAAT 924
Db 841 CTCTCTTTTCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATATGCTTATGCAAT 900
QY 925 TGTGTTTGTGCGGT 939
Db 901 TGTGTTTGTGCGGT 915

RESULT 13
ABZ59171
ID ABZ59171 standard; DNA; 918 BP.
XX
AC ABZ59171;
XX
DT 28-APR-2003 (first entry)
XX
DE Human TGR343 protein encoding DNA.
XX
KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antidiabetic; neuroprotective; cerebroprotective; nephroprotective;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "TGR343"
XX
PN W02003004678-A2.
XX
PD 16-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020860.
XX
PR 03-JUL-2001; 2001US-0302800P.
XX
PA (TUL-) TULARIK INC.
XX
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX
DR WPI; 2003-210368/20.
DR P-PSDB; ABP71378.
XX
XX
PT New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.
XX
PS
XX
PS Claim 7; Page 61; 74pp; English.
XX
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombinant methodology. The polypeptides are useful for screening or
CC identifying modulators of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR343
CC protein encoding DNA
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 97.3%; Score 913.4; DB 8; Length 918;
Best Local Similarity 99.9%; Pred. No. 1.9e-260;

Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 ATGCTGCGCAATATACCTCCAGGAATTCCTTTCGATCTTATATGACACCCCACTTA 84
Db 1 ATGCTGCGCAATATACCTCCAGGAATTCCTTTCGATCTTATATGACACCCCACTTA 60
QY 85 ATGAGCCCTTATCTTATATGATGCTTATATGAGGCGGTGCTGCTGATCTTTCCTTTTC 144
Db 61 ATGAGCCCTTATCTTATATGATGCTTATATGAGGCGGTGCTGCTGATCTTTCCTTTTC 120
QY 145 CTCTGCTGAAATATGACACCCCGGTGATGACACCAATGAGCGGTCTTAATCTTGATGATG 204
Db 121 CTCTGCTGAAATATGACACCCCGGTGATGACACCAATGAGCGGTCTTAATCTTGATGATG 180
QY 205 GTCCACAGCGTTTTCCTGCTGACAGTGCATTTGCTTACCTTCACTCAATCAAGAACT 264
Db 181 GTCCACAGCGTTTTCCTGCTGACAGTGCATTTGCTTACCTTCACTCAATCAAGAACT 240
QY 265 TGGATGTTTGGGCGTCCCTCTGCAATTTTGATGAGTGCATGCTGCAATCCCAATGTAC 324
Db 241 TGGATGTTTGGGCGTCCCTCTGCAATTTTGATGAGTGCATGCTGCAATCCCAATGTAC 300
QY 325 CTCACTTCTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 384
Db 301 CTCACTTCTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 385 AAAGCAAAAGTGAATCTTACAGAAAATGATGATGATGATGATGATGATGATGATGATG 444
Db 361 AAAGCAAAAGTGAATCTTACAGAAAATGATGATGATGATGATGATGATGATGATGATG 420
QY 445 ACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 504
Db 421 ACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 505 TACATATGAGAGCACTGTTTAAATTTCAAAAGAGCTTCAATATATGATGATGATGATG 564
Db 481 TACATATGAGAGCACTGTTTAAATTTCAAAAGAGCTTCAATATATGATGATGATGATG 540
QY 565 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624
Db 541 ATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 625 GTCTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684
Db 601 GTCTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 685 TTCTGGGCTCAGCTGAAACCTATTTTATATGAGGCTCATCTGTTGTTTCTTCTCC 744
Db 661 TTCTGGGCTCAGCTGAAACCTATTTTATATGAGGCTCATCTGTTGTTTCTTCTCC 720
QY 745 TACCACTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 804
Db 721 TACCACTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 805 AAGTTGCAATTTTAAACGAAATCTTCTGAGTGTAACAGCAATTAGCTGATGATTTG 864
Db 781 AAGTTGCAATTTTAAACGAAATCTTCTGAGTGTAACAGCAATTAGCTGATGATTTG 840
QY 865 CTCTCTTTTCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATATGCTTATGCAAT 924
Db 841 CTCTCTTTTCTTTGGGGGAAGCATGTGTTTAAGCAAAAGATATATGCTTATGCAAT 900
QY 925 TGTGTTTGTGCGGT 939
Db 901 TGTGTTTGTGCGGT 915

RESULT 14
ADO28919
ID ADO28919 standard; cDNA; 918 BP.
XX
AC ADO28919;
XX

DT 29-JUL-2004 (first entry)
XX
DE Human novel GPCR PGR13 polynucleotide, SEQ ID NO:18.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; autonomic;
KW cytoskeletal; antiinflammatory; vasotropic; antianginal; antirhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; anticancer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200404000-A2.
PN
XX 13-MAY-2004.
PD
XX
XX 09-SEP-2003; 2003WO-US028226.
PF
XX
XX 09-SEP-2002; 2002US-0409303P.
PR
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
PA
XX
PI Galitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F,
PI Medisen L, McIlwain KL, Pavlova KM, Vasiliadis D, Zeng H;
XX
XX WPI; 2004-390329/36.
DR P-PSDB; ADO28918.
XX
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 13; SEQ ID NO 18; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune diseases or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding

CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIP0 at
CC ftp.wipo.int/pub/published_pcc_sequences.
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Query Match 97.3%; Score 913.4; DB 12; Length 918;
Best Local Similarity 99.9%; Pred. No. 1.9e-260;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 ATGCCCTGACCAATATCTCCAGAAATTCCTTGGCATCTATATGACACCCCACTTA 84
DB 1 ATGCTGGCCACAAATATCTCCAGAAATTCCTTGGCATCTATATGACACCCCACTTA 60
QY 85 ATAGAGCTCTACTTCAATAGTCTATATGGCGGGCTGGTGGTGTCAATTCCTTTTC 144
DB 61 ATCAGGCTCTACTTCAATAGTCTATATGGCGGGCTGGTGGTGTCAATTCCTTTTC 120
QY 145 CTCCTGGTGAATAATGAAACCCGGTCAGTGACACCATGAGCGGTCAATTAATTTGGTG 204
DB 121 CTCCTGGTGAATAATGAAACCCGGTCAGTGACACCATGAGCGGTCAATTAATTTGGTG 180
QY 205 GTCCACAGCGTTTTCCTGCTGACAGTCCATTTGGCTTGAACCTTCAATCAAGAAAGCT 264
DB 181 GTCCACAGCGTTTTCCTGCTGACAGTCCATTTGGCTTGAACCTTCAATCAAGAAAGCT 240
QY 265 TGGATGTTGGGCTGCGCTTTCGCAAAATTTGAGTGCATGTGACATCCACATGTAC 324
DB 241 TGGATGTTGGGCTGCGCTTTCGCAAAATTTGAGTGCATGTGACATCCACATGTAC 300
QY 325 CTCAGGTTCCATATTCATGATGGTATCTGTGACACCATGATTCCTTCTTCAAGTGC 384
DB 301 CTCAGGTTCCATATTCATGATGGTATCTGTGACACCATGATTCCTTCTTCAAGTGC 360
QY 385 AAAGACAAAGTGAATTTCAAGAAATTCGATGCTGTGGCTGCGCATGCTGGCATGTG 444
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QY 445 AGCGTGTATGTCATTTGTGGTACCCCGTGTGTCTCCCGATGATGATTCATGAGAA 504
DB 421 AGCGTGTATGTCATTTGTGGTACCCCGTGTGTCTCCCGATGATGATTCATGAGAA 480
QY 505 TACAATGAGAGACAGTGTAAATTTCAAAAGAGCTTGCTTACATATGTAAGAAATC 564
DB 481 TACAATGAGAGACAGTGTAAATTTCAAAAGAGCTTGCTTACATATGTAAGAAATC 540
QY 565 ATCAACTATATGATATGATATTTTGTATGACCGTGTGTGATTTGTGTTGCTTCCAG 624
DB 541 ATCAACTATATGATATGATATTTTGTATGACCGTGTGTGATTTGTGTTGCTTCCAG 600
QY 625 GTTTCATCATATGATATGATATGATGACGAGCATGACCTTATATCCACAGAGAG 684
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QY 745 TACCACTTTTATAGATCTATTAATTTGATGAGCATTCATGCTGTAGAC 804
DB 721 TACCACTTTTATAGATCTATTAATTTGATGAGCATTCATGCTGTAGAC 780
QY 805 AAGGTGCAATTTATACGAAATCTTCTGAGTGAACGCAATTAAGTGCATATGTTTG 864
DB 781 AAGGTGCAATTTATACGAAATCTTCTGAGTGAACGCAATTAAGTGCATATGTTTG 840
QY 865 CTCTCTCTTGTCTTTGGGGAAGCCATGAGTTTAAAGCAAAAGTAATGGCTTAATGAAAT 924
DB 841 CTCTCTCTTGTCTTTGGGGAAGCCATGAGTTTAAAGCAAAAGTAATGGCTTAATGAAAT 900
QY 925 TGTGTTTGTGCGGT 939
|||||

Db 901 TGTGTTTGTGCCGT 915

RESULT 15

ID	standard; DNA; 1040 BP.
AA157070	

AC AAL57070;

DT 17-SEP-2003 (first entry)

Human G-protein coupled receptor GAVE18 DNA sequence

KM Human G-protein coupled receptor GAVR19; signal transduction;
KM inflammation; physiological immunological response; antiinflammatory;
KM antisthmatic; antirheumatic; antiallergic; antitense therapy;
KM chromosomal mapping; tissue typing; forensic biology;
KM predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
KM rheumatoid arthritis; gene; ds.

OS Homo sapiens

FH	Key	Location/Qualifiers
FT	CDS	1. .918

```

FT      /product= "GAVE18 protein"
.....

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PN WO2003042399-A2.

PD 22-MAY-2003

08-NOV-2002; 2002WO-US035887.

PR 22-MAR-2002; 2002GB-00006891.

PA (AVET) AVENTIS PHARM INC.

PI Eishengdrel H, Cai J, F

DR WPI; 2003-457496/43.

XX

PT polypeptide, used

PT rheumatoid arthritis.

PS Claim 1; Fig 5; 88pp; English

This invention relates

the physiological im-

CC antiinflammatory, antirheumatic or antiarthritic. The

antibodies may be useful in screening assays, detection assays (for example chromosomal mapping, tissue typing or forensic biology), or predictive medicine (for example diagnostic assays), prognostic assays, monitoring clinical trials and pharmacogenomics. The nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse agonist and antagonist are also useful for preventing and treating a disease or disorder associated with aberrant expression or activity of GAVE18, such as inflammation and immunological-related diseases or disorders, for example asthma, chronic obstructive pulmonary disease or rheumatoid arthritis. The present sequence is the DNA sequence encoding the GAVE18 protein of the invention

SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;

Query Match	97.3%;	Score 913.4;	DB 9;	Length 1040;
Best Local Similarity	99.9%;	Pred. No. 2e-260;		

Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	25	ATGCTGGGCAAAATCTTCAGGAATTCCTCTTGGATCTATATGTGACACCCACTTA	84
Db	1	ATGCTGGGCAAAATCTTCAGGAATTCCTCTTGGATCTATATGTGACACCCACTTA	60
QY	85	ATGAGCTCTACTTCAATGAGTCTTATATGGCGGAGCTGGTGGGTGCATTTCCATTCCTTTTC	14
Db	61	ATGAGCTCTACTTCAATGAGTCTTATATGGCGGAGCTGGTGGGTGCATTTCCATTCCTTTTC	12
QY	145	CTCCTGGTGAANAATGAAACAACCGGTGATGACACCAATGGCGGTCAATTAACTTTGGTGGTG	20
Db	121	CTCCTGGTGAANAATGAAACAACCGGTGATGACACCAATGGCGGTCAATTAACTTTGGTGGTG	18
QY	205	GTCCACAGCGTTTTTTCTGCTGACAGTGGCAATTTGCGTTGACCTTACCTCATCAAGAAAGCT	26
Db	181	GTCCACAGCGTTTTTTCTGCTGACAGTGGCAATTTGCGTTGACCTTACCTCATCAAGAAAGCT	24
QY	265	TGATATGTTGGGCTGCGCTTTCTTGCAAAATTTGTGATGATGCCATGCTGACATCCATGTAAC	32
Db	241	TGATATGTTGGGCTGCGCTTTCTTGCAAAATTTGTGATGATGCCATGCTGACATCCATGTAAC	30
QY	325	CTCACGTTCCATTTCTATATGTGGTGAATCTGTGTCACCAATATCTATCTTTCAAGTGC	38
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QY	385	AAAGACAAAGTGAATTTCTACAGAAAACGTACATGCGTGGCGGACAGTGGCGGATGGG	44
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QY	445	ACGCTGGATATGTCAATGTGGTACCCCTGATGTCTCCCGATATGAAATCCATGAGAA	50
Db	421	ACGCTGGATATGTCAATGTGGTACCCCTGATGTCTCCCGATATGAAATCCATGAGAA	48
QY	505	TACAAATGAGAGAGACGTTTTTAAATTTACAAAGAAGCTTGCTTACACATATGTGAAAATC	56
Db	481	TACAAATGAGAGAGACGTTTTTAAATTTACAAAGAAGCTTGCTTACACATATGTGAAAATC	54
QY	565	ATCAACATATATGATAGTCAATTTTTGTGCATAGCGGTGGCGTGAATCTGTGGTCTTCCAG	62
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QY	625	GTCCTCATCATTAATGTGTGATGTGTGACGAAGCTACGCCACTCTTTACTATCCACAGGAG	68
Db	601	GTCCTCATCATTAATGTGTGATGTGTGACGAAGCTACGCCACTCTTTACTATCCACAGGAG	66
QY	685	TTCTGGAGCTCAGCTGAAAAACCTAATTTTTTATATAGGGGTCAATCTTGTGTTCCTTCCC	74
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QY	745	TACCAATTTCTTTAAGATCTATATCTTGAATGTGTGAGAGCATTCGAATGCCCTGTAGAGAC	80
Db	721	TACCAATTTCTTTAAGATCTATATCTTGAATGTGTGAGAGCATTCGAATGCCCTGTAGAGAC	78
QY	805	AAGGTGCAATTTATACGAATCTTCTTGAATGTGACGACCAATATAGCTGATATATTTG	86
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QY	865	CTTCTCTTTTGTCTTTGGGGGAAAGCAATGGTTTAAAGCAAAAGATATATTTGGCTTATGAAAT	92
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QY	925	TGTGTTTTTGTGCGGT 939	
Db	901	TGTGTTTTTGTGCGGT 915	

Search completed: September 10, 2005, 04:04:52
Job time : 550.362 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 01:56:38 ; Search time 3394.79 Seconds
(without alignments)
10528.586 Million cell updates/sec

Title: US-10-085-233B-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_est1: *
2: gb_est2: *
3: gb_hnc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est1: *
9: gb_est2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678.8	72.3	694	7	CO918710 AGENCOURT
2	588.2	62.6	717	7	CO918845 AGENCOURT
3	537.4	57.2	684	9	AG145972 Pan trogl
4	415.8	44.3	772	2	BF160725 601769127
5	346.8	36.9	580	8	AZ554824 RPCI-23-2
6	338	36.0	455	8	AQ888495 HS_3162_B
7	325.8	34.7	678	5	BA952455 DKFZP/8IN
8	237.2	25.3	646	5	BG862323 602796201
9	203	21.6	499	6	CD699779 EST16303
10	181	19.3	649	4	BG461295 RST44080
11	162	17.3	283	4	BG221739 RST41554
12	146.8	15.6	478	4	BG145683 mac33c07.
13	146.2	15.6	2774	3	AK041317 Mus muscu
14	142	15.1	834	1	AJ455645 AJ455645
15	111	11.8	680	6	CA355790 627748 NC
16	86.4	9.2	661	6	BY748361 BY748361
17	82	8.7	705	7	CN793065 4128026 B
18	76.2	8.1	679	6	CD469227 Leuko52.2
19	72.2	7.7	733	6	CA050323 88a1x9b52
20	71.4	7.6	648	6	CB514250 88a1x9b54
21	70	7.5	659	5	BQ563030 H4079D04-
22	69.8	7.4	879	9	AY410745 Homo sapi
23	69.4	7.4	866	6	CD246184 AGENCOURT

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26	68.6	7.3	542	6	CA965628	CA965628 CcIX05a15
27	67	7.1	672	7	CO957761	CO957761 AGENCOURT
28	64.4	6.9	671	6	BY752012	BY752012 BY752012
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32	60	6.4	450	6	CA576592	CA576592 K0647B04-
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36	59.8	6.4	2959	3	AK079529	AK079529 Mus muscu
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38	58	6.2	718	7	CO570572	CO570572 AGENCOURT
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40	58	6.2	791	6	CD559647	CD559647 AGENCOURT
41	58	6.2	792	6	CD559648	CD559648 AGENCOURT
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44	55.8	5.9	653	2	BB636445	BB636445 BB636445
45	55.6	5.9	730	7	CF147825	CF147825 AGENCOURT

ALIGNMENTS

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LOCUS AGENCOURT 30488597 NIH MGC 145 Homo sapiens CDNA clone
DEFINITION IMAGE:7211820 5', mRNA-sequence.
ACCESSION CO918710
VERSION CO918710.1 GI:51266406
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-remail.nih.gov
Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB15 row: c column: 10
High quality sequence stop: 489.
Location/Qualifiers

FEATURES

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ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat

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DB	129	TTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAATTGGTTTGGGC	70
QY	937	CCT 939	
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DEFINITION			
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KEYWORDS			
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AUTHORS			
TITLE			
JOURNAL			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
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DB	10	AAAAAATCCGGGCTTTCTACAGAAAATTCGATGCTGTGGCTGCACGCTGGCATGTGG	69
QY	445	ACGCTGTGATTTGCATTTGTGGTACCCCTGGTGTCTCCGGTATGGAATTCATGAGGAA	504
DB	70	ACGCTGTGATTTGCATTTGTGGTACCCCTGGTGTCTCCGGTATGGAATTCATGAGGAA	129
QY	505	TACAAATGAGAGCACTGTTTTAAATTTACAAAGACTTGCTTACATATGTGAAATC	564
DB	130	TACAAATGAGAGCACTGTTTTAAATTTACAAAGACTTGCTTACATATGTGAAATC	189
QY	565	ATCAACTATATGATATGATATTTTGTCTATACCGCTGTGATTTCTGTGCTTCCAG	624

Db	130	ATCAACTAATAGTAGTCATTCTTTGTGTAACACCGTGTGTCGATCTTGTTGGTCTCCAG	245
Oy	625	GTCCTCATCATTATGTGTGAGTGCAGAAGCTACGCCACTCTTATTAATACCACAGGAG	684
Db	250	GCTTCATCATTAATGTGTATGTGTGCAGAAAGCTACGCCACTCTTACTATATCCACAAGAG	309
Oy	665	TTCTGGGCTCAGCTCGAAAAACCTATTTTTTATAGGGGTCATCCTGTTGTTCCCTCCC	744
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DEFINITION	601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5'		
ACCESSION	BF160725		
VERSION	BF160725.1	GI:11040832	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs-rc@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CNLA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM9196 row: f column: 07 High quality sequence stop: 634. Location/Qualifiers		
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	Stem cell origin."		
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	/clone_1lb="NCI_CGAP_Lu29"		
	/note="Organ: lung; Vector: pCMV-Sport5; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. library constructed by life technologies. Investigator providing samples: Gilbert Smith, NIH"		
ORIGIN			
Query Match	44.3%	Score 415.8;	DB 2; Length 772;
Best Local Similarity	79.2%;	Pred. No. 4.2e-106;	

Matches 544; Conservative 0; Mismatches 137; Indels 6; Gaps 4;

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QY 295 GTGAGTGCATGCGCATCCATCCATGATCTCACTGCTTCTATTTATGTTGATCTG 354
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QY 772 AATGTTGTGACGATTCATGCTGT 798
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RESULT 5
AZ554824 580 bp DNA linear GSS 20-NOV-2000
LOCUS
DEFINITION
RPECI-23-211E13, TV RPECI-23 Mus musculus genomic clone
RPECI-23-211E13, genomic survey sequence.
ACCESSION
AZ554824
VERSION
AZ554824.1 GI:11234644
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S.,
Alinret, B., Levyn, M., McGann, S., Tsegeye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPECI-23
Unpublished (1999)
TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPECI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/orderingframe.html>)
or from ResGen ch Genetics (<http://resgen.com>). BAC end page:
http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 211 row: E column: 13
Seq primer: 17
Class: BAC ends.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPECI-23-211E13"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPECI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

FEATURES

source

ORIGIN

Query Match 36.9%; Score 346.8; DB 8; Length 580;
Best Local Similarity 79.6%; Pred. No. 1.3e-86;
Matches 422; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

```
QY 410 AACTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AATGATCATCAGTGTGTGCAAGTTCT- GCTGTGCTTCTGTGATGTTATTTGTTGTC 59
QY 470 CCTGTGTTCTCCGGTATGGAATTCATGAGAAATACATAGAGACCTGTTTAAT 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 CCTGTGTTCTCCGGTATGGAATTCATGAGAAATACATAGAGACCTGTTTAAT 119
QY 530 TTCACAAAGAGTGTGCTTACATATGTAATAATCATCAATATATGATGATCTTTG 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 TCCATTAAGAACTTGGCCATGATTTCTGTGCAAGTTATCACTATATGATGATCTTTG 179
QY 590 TCATAGCCGTGTGTGATTTCTGTGTGCTTCCAGGCTTTCATCATATATGATGATGTC 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 TCATAGCTGTGTGATTTCTGTGTGCTTCCAGGCTTTCATCATATATGATGATGTC 239
QY 650 AGAAGCTACGCCACTTTTACTATCCACACAGAGTTCGGGCTCAGCTGAGAAAACCTAT 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 GGAAGTTTGGCACTCTTCACTATCCACACAGAGTTCGGGCTCAGCTGAGAAAACCTAT 299
QY 710 TTTTATAGGGGCTATCTTGTGTTGTTCTTCCCTACAGTCTTTAGATCTATTA 769
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TCTTTATAGATATCATTTATTTGTTTCTTCCCTACAGTCTTTAGATCTATTA 359
QY 770 TGAATGTTGACGATTCATGCTGCTGAGAGAGAGTTCATTTATTAAGAAATCT 829
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTATTTTGTGGACATTCCTCAAGAGTGTAAAAACAAATTCATTTTATTAAGAAATCT 419
QY 830 TCTTATGTTTACAGCAATTTAGTGTGATTTGCTTCTTGTGTTGTTGTTGTTGTTG 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 TATTGAGCAACACAGCATACAGTGTGATTTGCTGTTTGTGTTTGTGTTGAGGAAACC 479
QY 890 ATTGTTTAAAGCAAAAGATATTTGGCTTATGAAATTTGTTTGGCGCT 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 ATTGGTTAAGCAAAAGATTTGACATGTGAAATTTGCTTTATGCTAT 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 6	
AQ888495	
LOCUS	
AQ888495	456 bp DNA linear GSS 10-NOV-1999
DEFINITION	HS_3162_B1_B01_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey sequence.
ACCESSION	AQ888495.1 GI:6344685
VERSION	GSS.
KEYWORDS	Homo sapiens (human)
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 456)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED	99380589
COMMENT	10449764 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hltsc.washington.edu Plate: 3162 Row: D Column: 1 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 456. FEATURES source location/Qualifiers 1..456 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Plate=3162 Col=1 Row=D" /sex="male" /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBelobAc11; BAC clones in E-Coli DH10B"
ORIGIN	
Query Match	36.0%; Score 338; DB 8; Length 456;
Best Local Similarity	97.3%; Pred. No. 3,6e-84;
Matches 364; Conservative 0; Mismatches 7; Indels 3; Gaps 2;	
DY	403 TACAGAAACGCAAGCTGTGGCGCCAGTGCCTGGCATGTGAGCGCTGGATGTGTAATT 462
Db	1 TAGCAAAAACTCAGATGCTGTGGCTGCCAGTGCTGCAATGTGAGCGCTGGATGTGTAATT 60
DY	463 GTGGTACCCTGTGTCTCTCCCGGTATGATTCATGAGAATAATGAAGACTGT 522
Db	61 GTGGTACCCCTGTGTCTCTCCCGGTATGATTCATGAGAATAATGAAGACTGT 120
DY	523 TTATAATTTCCAAAGAGCTTGCTTACATATGTGAAAAATCATCAAATATGATGATGTC 582
Db	121 TTATAATTTCCAAAGAGCTTGCTTACATATGTGAAAAATCATCAAATATGATGATGTC 180
DY	583 ATTATTGCAATAGCGGTGCTGTGATTCATGTTGGCTTTCCAGGCTTCATCATATGTTG 642
Db	181 ATTATTGCAATAGCGGTGCTGTGATTCATGTTGGCTTTCCAGGCTTCATCATATGTTG 240
DY	643 ATGTGTGAGAAGCTTAGCGCACTCTTTACTATCCACAGAGAGTTCTGGGCTCAGCTGAA 702
Db	241 ATGTGTGAGAAGCTTAGCGCACTCTTTACTATCCACAGAGAGTTCTGGGCTCAGCTGAA 300
DY	703 AACCTATTTTTAATAGGGGTGATCTCTGTTGTTTCTTCCCTACAGATCTTTAGGATC 762

Db	301	AAACCTATTTTATAGGGGTACCTCTTTGTTT-CTTCCCTACCACT--CTTAGATC	357
Qy	763	TATTACTTGAATGT	776
Db	358	TATTACTTGAATGT	371
RESULT 7			
LOCUS	BX952455	678 bp	mRNA
DEFINITION	DKFZP781N17197 r1 781 (synonym: hlcc4)	678 bp	linear EST 01-MAR-2004
ACCESSION	BX952455		
VERSION	BX952455.1		
KEYWORDS	EST.		
SOURCE	Human sapiens (human)		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.		
TITLE	EST (Wambutt,R., Heubner,D., Mewes,H.W., Well,B., Amid,C., et al.)		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: MIPS		
FEATURES	source		
source	1. .678		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="DKFZP781N17197"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/clone_lib="781 (synonym: hlcc4)"		
	/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIB; cDNA-collection"		
ORIGIN			
Query Match	34.7%;	Score 325.8;	DB 5; Length 678;
Best Local Similarity	99.1%;	Pred. No. 1,2e-80;	
Matches 327;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	7	AAATGACTTCCCAAGTATGCTGCGGCACAAATACCTCCAGAAATTCCTTGGGATCT	66
Db	349	ACAGGTGACTTCCCAAGTATGCTGCGGCACAAATACCTCCAGAAATTCCTTGGGATCT	408
Qy	67	ATATGTGACACCCCACTTAATCAGCCTTACTTCAATAGTGCTTAATGGCGGCTGTGGGT	126
Db	409	ATATGTGACACCCCACTTAATCAGCCTTACTTCAATAGTGCTTAATGGCGGCTGTGGGT	468
Qy	127	GTCATTTCCAAATCTTTTCCCTCGTGTGAAATGAACACCGGTCAGTACACCATGGCG	186
Db	469	GTCATTTCCAAATCTTTTCCCTCGTGTGAAATGAACACCGGTCAGTACACCATGGCG	528
Qy	187	GTCATTAACCTGTGTGTGTGTCACAGCGTITTTCTGTGTGACAGTGCATTTGCTTGACC	246
Db	529	GTCATTAACCTGTGTGTGTGTCACAGCGTITTTCTGTGTGACAGTGCATTTGCTTGACC	588
Qy	247	TACCTATCAAGAAGACTTGGATGTTTGGGCTGCGCTTTCGCAATTTTGAAGTGCATG	306
Db	589	TACCTATCAAGAAGACTTGGATGTTTGGGCTGCGCTTTCGCAATTTTGAAGTGCATG	648

QY 307 CTCACATCCACATGTAAGTCTACGTTCTCTA 336
|||||
Db 649 CTCACATCCACATGTAAGTCTACGTTCTCTA 678
|||||

RESULT 8
LOCUS BG862323 646 bp mRNA linear EST 29-MAY-2001
DEFINITION 602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
mRNA sequence.
ACCESSION BG862323
VERSION BG862323.1 GI:14212861
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furch
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM10828 row: b column: 01
High quality sequence stop: 644.
Location/Qualifiers
source
1..646
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:4917024"
/issue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furch,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

ORIGIN
Query Match 25.3%; Score 237.2; DB 4; Length 646;
Best Local Similarity 79.4%; Pred. No. 1.4e-55;
Matches 281; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 11 GTGACTCCGAAGTANGCCTGGCCACATACCTCCAGAAATTCCTCTTGAGATCCTATAG 70
|||||
Db 293 GTAAATGTTGAAGATGATGATATATATACCTTGAAATTCCTCTTGAGATCCTATAG 352
|||||

QY 71 TGAACCCCACTTAATCAGCCTCTACTCTATAGTCTTATTTGGCGGCTGTGGGTGTCA 130
|||||
Db 353 TGGCAGACCACTTAATCAGCCTCTACTCTATAGTCTTATTTGGCGGCTGTGGGTGTCA 412
|||||

QY 131 TTTCATCTTTCTCTCTGCTGTAATAATGAACACCCGCTGAGTGAACCACTGGCGGTCA 190
|||||
Db 413 TCTCCATCCGCTTCTCTGCTGTAATAATGAACACCTGAGTGAACCACTGGCGGTCA 472
|||||

QY 191 TTAACCTGTTGGTGTCCACAGCGTTTTCGCTGACAGTGCATTTGCTTGAACCTAC 250
|||||
Db 473 TCAACCTGTTGGTGTCCACAGCGTTTTCGCTGACAGTGCATTTGCTTGAACCTAC 532
|||||

QY 251 TCATCAAGAAGACTTGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGATGCCATGCTGC 310
|||||

Db 533 TCATCAAGAAGACTTGAGCTTTGATATACCTCTTGCAAAATTTGATGATGCATGTAC 592
|||||

QY 311 ACATCCACATGTAAGTCTACGTTCTCTATATGATGATCTCTGGTACACCAAT 364
|||||
Db 593 ATATCCACATGTAAGTCTACGTTCTCTATATGATGATCTCTGGTACACCAAT 646
|||||

RESULT 9
LOCUS CD699779 499 bp mRNA linear EST 25-JUN-2003
DEFINITION EST16303 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD699779
VERSION CD699779.1 GI:32229387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 499)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
source
1..499
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 21.6%; Score 203; DB 6; Length 499;
Best Local Similarity 100.0%; Pred. No. 6.1e-46;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GTGACTCCGAAGTATGCTCTGGCCACATATCTCCAGAAATTCCTTCCATCCTATAG 70
|||||
Db 297 GTGACTCCGAAGTATGCTCTGGCCACATATCTCCAGAAATTCCTTCCATCCTATAG 356
|||||

QY 71 TGAACCCCACTTAATCAGCCTCTACTCTATAGTCTTATTTGGCGGCTGTGGGTGTCA 130
|||||
Db 357 TGAACCCCACTTAATCAGCCTCTACTCTATAGTCTTATTTGGCGGCTGTGGGTGTCA 416
|||||

QY 131 TTTCATCTTTCTCTCTGCTGTAATAATGAACACCCGCTGAGTGAACCACTGGCGGTCA 190
|||||
Db 417 TTTCATCTTTCTCTCTGCTGTAATAATGAACACCCGCTGAGTGAACCACTGGCGGTCA 476
|||||

QY 191 TTAACCTGTTGGTGTCCACAGC 213
|||||
Db 477 TTAACCTGTTGGTGTCCACAGC 499
|||||

RESULT 10
LOCUS BG461295 649 bp mRNA linear EST 21-APR-2001
DEFINITION RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG461295
VERSION BG461295.1 GI:13749801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 649)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com.
Location/Qualifiers
1. 649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match 19.3%; Score 181; DB 4; Length 649;
Best Local Similarity 74.1%; Pred. No. 1.1e-39;
Matches 355; Conservative 0; Mismatches 50; Indels 74; Gaps 7;

ORIGIN

11 GTGACTTCCCAAGTATGCTGCGCCCAATACCTCCATTCCTTCGATCCTATAG 70
108 GTGACTTCCCAAGTATGCTGCGCCCAATACCTCCATTCCTTCGATCCTATAG 151
71 TGACACCCCACTTATGAGCTCTACTCATAGTGTATTTGGGGGCTGGTGGGTGCA 130
152 TGACACCCCACTTATGAGCTCTACTCATAGTGTATTTGGGGGCTGGTGGGTGCA 211
131 TTTCATTTCTTTCTCTCTGCTGTAATAAGAACCCGCTGATGACCAACATGCGGTCA 190
212 TTTCATTTCTTTCTCTCTGCTGTAATAAGAACCCGCTGATGACCAACATGCGGTCA 254
191 TTAACCTGTTGGTGTGTCACAGCGTTTCTTGTGTCAGATG-CGATTTGCTTACCTAC 249
255 TTAACCTGTTGGTGTGTCACAGCGTTTCTTGTGTCAGATG-CGATTTGCTTACCTAC 314
250 CTGATCAAGAAGATTGGATGTTGGGCTGCTTGTGCAAAATTGGAGGCGCATGCTG 309
315 C-----CTTTGGGCTGCTTGTGCAAAATTGGAGGCGCATGCTG 356
310 CACATCCACATGTACTCAGCTTCT-ATTCTATGTTGGTATCCTGCTACACAGATACCT 368
357 AACATTCACATGTACTCAGATCTTAATCTATGAGGTATCTCGCGCGCGAT----- 412
369 CATCTTCTTCAAGTGCAAGCAAGATGGAATTCTACAGAAACTGCATGCTGTGCTGC 428
413 -----CAAGCAAAAGGGAAGCTT-TACAGAGTGTGCGCCCGGAGGTGTC 455
429 CAGTGTGCGCATGTTGAGCGCTGTTGATTTGTCATTTGTTGCTGTTGCTCCCGGT 487
456 CAGAGCTGGCATGTGAGCGCTGTTGATTTGTCATGCGCGCGCCCGCGGTGTTCCGGGT 514

RESULT 11
BG221739
LOCUS BG221739 283 bp mRNA linear EST 21-Apr-2001

DEFINITION RST41554 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG221739
VERSION BG221739.1 GI:13747760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 233.
Location/Qualifiers
1. 283
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match 17.3%; Score 162; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2e-34;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

11 GTGACTTCCCAAGTATGCTGCGCCCAATACCTCCATTCCTTCGATCCTATAG 70
122 GTGACTTCCCAAGTATGCTGCGCCCAATACCTCCATTCCTTCGATCCTATAG 181
71 TGACACCCCACTTATGAGCTCTACTCATAGTGTATTTGGGGGCTGGTGGGTGCA 130
182 TGACACCCCACTTATGAGCTCTACTCATAGTGTATTTGGGGGCTGGTGGGTGCA 241
131 TTTCATTTCTTTCTCTCTGCTGTAATAAGAACCCGCTGATGACCAACATGCGGTCA 172
242 TTTCATTTCTTTCTCTCTGCTGTAATAAGAACCCGCTGATGACCAACATGCGGTCA 283

RESULT 12
BG145683
LOCUS BG145683 478 bp mRNA linear EST 01-FEB-2001
DEFINITION mac33c07.y1 Soares mouse 3NDMS Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.
ACCESSION BG145683
VERSION BG145683.1 GI:12649019
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 478)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

/dev_stage="adult"
311..1210
/note="unnamed protein product: hypothetical
Rhodopsin-like GPCR superfamily containing protein
(InterPro|IPR00276, evidence: InterPro)
putative"
/codon_start=1
/protein_id="BAC30904.1"
/db_xref="GI:26334373"
/translation="MDPMDVIVSNGSSVPMABOYCDACHALITLTVASVPEGFT
VGTVMSSHMFKNQSMATITITITVLSLISLPFLSYFSVWVLGSPFCM
VSGVIGHMYLTF1EYVAIVTLRLIYFKLQOQOLQKRAVALSIIIVTGSFELP
IFPLOYGSDPSYEOQCEPFHKSINRDIILNYSIIIVMTTVLLFLIQAVILH
LIRAYMDMAHOBEOIRAOKISFFELVIVVCFIPHAFRVYFIQNPFEQNSLILVN
EICVALAFPCCLMLCRIGSVIH"

Query Match 15.6%; Score 146.2; DB 3; Length 2774;
Best Local Similarity 51.7%; Pred. No. 1.5e-29;
Matches 412; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

QY 101 TAGTGCTATTTGGGGGCTGGTGGTGCATTTTCATTTCTTCTCTGCGTGAATAAATGA 160
DB 423 TGGTCTTCTTTGGAGGACCGGTGMAACAGTTATGATGTCACACATGATGTTCAAGAGA 482
QY 161 ACACCGGTCAGTACACACACGCGGTCACTTAACCTGGTGGTGCACAGGCTTTTC 220
DB 483 ATTGCCATCAATGATTTGCCATCTATCATCTTAATATCATTTGTTGCACCTCCCTTCTCC 542
QY 221 TGCTGACAGTGCATTTGCTTGCCTGACCTCATCAAGAAAGACTTGATGTTGGGCTGC 280
DB 543 TGATTAGTGCATTTCCGCTCAGTACATTAATTTCTAGACAGTCTGGAACCTTGGGCTT 602
QY 281 CTTTGCATTAATTTGATGTCATGCTGCACATCAATGATCTCACTTCATTTCT 340
DB 603 TTACTGCGCAATGGTATGAGGCTCATATATGTCATATGATCTTACCTTCATTTT 662
QY 341 ATGAGGATCTCGTACACAGAACTCATCTTCTCAAGTGGAAAGAAAGTGAAT 400
DB 663 ATGTGGCATTTGATCTTCTGCGCTGCATCTATTTTAAG---AACTGCAATATGCAAC 719
QY 401 TCTACAGAAAATGTCATGCTGTGGCTGCAGTGTGCATGTGGACGCTGTGATTTGCA 460
DB 720 AGTTACAAAAGTTCATGCGCGTGGCTTAAGTATTTATTTGGGTGACAGAAAGCTTCA 779
QY 461 TTGTGTATCCCTGGTGTCTCCCGGTATGAAATTCATGAGAAATACATGAGAGAC- 519
DB 780 TCTTTTACCAATATTTTTCATATATGSCACAGATCCAGTTATACAGACCAACAGC 839
QY 520 --TGTTTAAATTTCAAGAGGTTGCTTACACATATGGAATATCAATCATATATGA 577
DB 840 GGTGCTTGAATTCATTAATCTCTCACTCCAGGACATCATCATATAAATCATTTCTA 899
QY 578 TAGTCATTTTGTATAGCCGTGTGTGTGATTCGTGTGCTTCCAGGCTTTCATCATTA 637
DB 900 TAATGTATTAATGATGACAAAGTTCTGCTCTTCTTGATACAGATGGCTGTCTATTC 959
QY 638 TGTGATGTGCAAGAGTACGCCACTTTTACTATTCACACAGAGTTCTGGGCTCAGC 697
DB 960 TTCAATTTGATTAAGAGCTATGAGCTATATGAGGCGCATCAAGAGTACAGAGCTCAA 1019
QY 698 TGAAGAAACCTATTTTATAGGGGTATCTTGTGTTGTTCCCTTCCATCAAGTTCTTGA 757
DB 1020 TCAAGAGTTTCTTCTGCTGTGTGATGATGTGTGCTTTATATCCCAACATGCAATCA 1079
QY 758 GATATTAATTTGATGATGTTGACGATTCATATGCTGTAGACAGCAAGTGTGCAATTT 817
DB 1080 GGGTATATTTTATTCAAAATTTTCCAGAGCAAGAAATTTCT-----AAGTTAATCTGT 1133
QY 818 ATTAAGAAATCTTCTGAGTGAACAGCAATTAAGCTGTATGATTTGCTTCTCTTGTCT 877
DB 1134 ACAATGAATCTGTGTGCTTAAAGCTTTCTGCTGCTGATATGTTATGTTTCAATAG 1193

QY 878 TTGGGGGAAGCCATTGG 894
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RESULT 14
AJ455645 834 bp mRNA linear EST 22-APR-2002
AJ455645 riken1 Gallus gallus cdna clone 6b4r1, mRNA sequence.
AJ455645
DEFINITION
AJ455645
ACCESSION
AJ455645.1 GI:20265741
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Gallus gallus
Bukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 834)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: <http://genetics.hpi.uni-hamburg.de/dt4dest.html>.
Location/Qualifiers
1..834
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="6b4r1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_1ib="riken1"
/note="CB inbred strain"

ORIGIN
Query Match 15.1%; Score 142; DB 1; Length 834;
Best Local Similarity 64.1%; Pred. No. 1.4e-28;
Matches 225; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

QY 81 CTTAATCAGCCTTACTTATGATGCTTATTTGGCGGCGTGGTGGTCAATTTCCATTTCC 140
DB 438 CTGATTAATCTGTACTCATGTCCTTCTGAGGTGGATGATTCACCTGCAATGTC 497
QY 141 TTCTCTCTGTGAAATGAACACCGGTCAAGTACCAACATGCGGTATTAATTTGGT 200
DB 498 ATTGTGCTGTGCAAGATGAACAGTCTGTGTGACCACTACAGCATATTAATCTAGT 557
QY 201 GGTGTCCACAGCGTTTTCGTGTGACAGTGCATTTGCTTGAACCTTCACTCAAGAA 260
DB 558 TGTGTACATGTCCTCTTCTCTCCACAGTGCCTTCCGTGACATCATATGTCATTA 617
QY 261 GACTTGAGTTGGTGGCTGCGCTTGCAGAAATTTGATGATGTCAGCTGACATCCACAT 320
DB 618 GAGTGAATCTTCCACATACATCTCTGTAATGAGTGTATGAGTGCACATCCACAT 677
QY 321 GTAATCAGCTTCTTATTTATGATGATTCCTGTGACCAAGATACCTGATC-TTCTTCA 379
DB 678 GATATTTGATCTTCTTATTTCTAGCTATACATCTGATGATCCGAGNGATGGCTTTCTTC 737
QY 380 AGTCAAGAACAAAGTGAATTTCAAGAAAATGATGATGCTGTGCTGCCA 430
DB 738 AATGGAAGAACANGTAGAGTTTATAGAAACTTCATCATCTGCTTCA 788

RESULT 15
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CA355790 627748 NCCMA 1RT Oncohyunchus myliss cdna clone 1RT8K09_A_F05 5',
DEFINITION
mRNA sequence.
ACCESSION
CA355790

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:36:04 ; Search time 170.402 Seconds
(without alignments)
9016.710 Million cell updates/sec

Title: US-10-085-233B-3

Perfect score: 939

Sequence: 1 atgcaaaatgctgacttccc.....ggaatgtgtgtgtgtgcgcg 939

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	76.4	8.1	1133	US-09-826-509-540	Sequence 540, App
2	76.4	8.1	1805	US-08-405-271A-18	Sequence 18, Appl
3	76.4	8.1	1973	US-09-016-434-1391	Sequence 1391, Ap
4	76.4	8.1	1973	US-09-023-655-1417	Sequence 1417, Ap
5	76.4	8.1	3205	US-09-976-594-171	Sequence 171, Appl
6	73.2	7.8	1134	US-09-743-871B-13	Sequence 13, Appl
7	70.2	7.5	1177	US-09-743-871B-13	Sequence 13, Appl
8	62.8	6.7	1273	US-09-910-695-9	Sequence 9, Appl
9	59.8	6.4	1330	US-08-147-592A-5	Sequence 5, Appl
10	59.8	6.4	1330	US-08-282-694A-5	Sequence 5, Appl
11	59.8	6.4	1367	US-08-889-108-16	Sequence 16, Appl
12	59.8	6.4	1567	PCT-US94-10358-16	Sequence 16, Appl
13	59.8	6.4	2600	US-08-986-209A-1	Sequence 1, Appl
14	59.8	6.4	2706	US-08-454-549-1	Sequence 1, Appl
15	59.8	6.4	2706	US-08-454-552-1	Sequence 1, Appl
16	59.8	6.4	2706	US-08-676-351-1	Sequence 1, Appl
17	59.4	6.3	1143	US-09-826-509-542	Sequence 542, App
18	59.4	6.3	1182	US-09-016-434-1417	Sequence 1417, Ap
19	58.2	6.2	1452	US-08-149-093A-3	Sequence 3, Appl
20	58.2	6.2	1452	US-08-911-245-3	Sequence 3, Appl
21	58.2	6.2	1452	US-08-553-058C-3	Sequence 3, Appl
22	58.2	6.2	1452	US-08-514-451A-3	Sequence 3, Appl
23	58.2	6.2	1452	US-09-170-331-3	Sequence 3, Appl
24	58.2	6.2	1452	US-09-510-473-3	Sequence 3, Appl
25	58.2	6.2	1452	US-09-048-916B-3	Sequence 3, Appl
26	58.2	6.2	1002	US-09-170-496D-15	Sequence 15, Appl
27	58.2	6.2	1002	US-09-170-496D-171	Sequence 171, App

28	58	6.2	1518	1	US-08-148-215A-3	Sequence 3, Appl
29	58	6.2	1518	4	US-09-016-434-1480	Sequence 1480, Ap
30	57.8	6.2	1142	3	US-08-765-743-1	Sequence 1, Appl
31	57.8	6.2	1143	4	US-09-341-446B-1	Sequence 1, Appl
32	57.8	6.2	1284	4	US-09-341-446B-1	Sequence 3, Appl
33	55	5.9	1000	3	US-08-147-592A-11	Sequence 11, Appl
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35	54.2	5.8	1155	3	US-09-053-866-3	Sequence 3, Appl
36	54.2	5.8	1155	3	US-09-479-130-3	Sequence 3, Appl
37	54.2	5.8	1155	4	US-09-472-130A-3	Sequence 3, Appl
38	54	5.8	1257	4	US-09-826-509-572	Sequence 572, App
39	54	5.8	1296	1	US-07-816-283-9	Sequence 9, Appl
40	54	5.8	1296	4	US-08-417-103-9	Sequence 9, Appl
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42	52	5.5	1223	4	US-09-743-871B-11	Sequence 11, Appl
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44	50.4	5.4	1256	4	US-09-743-871B-9	Sequence 9, Appl
45	50.4	5.4	2634	4	US-09-743-871B-8	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-09-826-509-540
; Sequence 540, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-tin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 540
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-826-509-540

Query Match      8.1%; Score 76.4; DB 4; Length 1113;
Best Local Similarity 46.7%; Pred. No. 1.1e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 178 ACCATGCGGTGATTAATCTGTGTGTGTGTCACAGCGTTTCTGTGACAGTGCATT 237
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RESULT 2
US-08-405-271A-18
; Sequence 18, Application US/08405271A
; Patent No. 6432652
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,271A
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFOERSMWH
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1119
; US-08-405-271A-18

Query Match 8.1%; Score 76.4; DB 3; Length 1805;
Best Local Similarity 46.7%; Pred. No. 1.5e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy 118 CTGGTGGGTCTATTTCCATCTTTCTCTCTGTAATAAGACCCGGTCAAGTACC 177
Db 208 CTGGGGAATCTGCTTGTCATGTCATCTCTAGGACACCAAAATGAAGACGACCC 267
Qy 178 ACCATGGCGGTCAATTAATCTGTGTGTGTCACAGCGTTTCTGCTGACAGTCCATT 237
Db 268 AATATTATCATCTTTAACTCGGCCCTGGCGACACATCTGTCTGTGACGCTGCCCTTC 327
Qy 238 CGCTTGACTCACTCATCAAGAAAGACTTGAGTGTGGGCTGCCCTTCTGCAAAATTTGTG 297

Db 328 CAGGCAACGACATCTCTCTGGGCTTCTTGCCGTTGGGAATGCCCTGTGCAAGACAGTC 387
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RESULT 3
US-09-016-434-1391
; Sequence 1391, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seihamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: 9471316
US-09-016-434-1391

Query Match 8.1%; Score 76.4; DB 4; Length 1973;
Best Local Similarity 46.7%; Pred. No. 1.5e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 178 ACCATGCGGTCATTAACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
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DB 436 AATATTACATCTTTAACTGCGCCCTGCGGACACTGCTGCTGCTGCTGCTGCTGCT 495
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QY 238 GCTTGACCTTACCTCATCAAGAAAGACTTGATGTTGGCTGCTGCTGCTGCTGCT 297
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DB 496 CAGGACACGACATCTCTGCGCTCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCT 555
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QY 358 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGAAAGTGAATCTACAGAAACTGCAT 417
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DB 616 GATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675
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DB 676 GCCCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
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QY 478 GTCTCCCGGTATGAAATCCATGAGAAATGATGATGATGATGATGATGATGATGAT 537
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DB 736 ATCATGGGCTGCGACAGTGCAGAGATGAAGATGAGATGAGATGAGATGAGATGAGAT 795
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QY 538 GAGCTTGCTTACATATGATGAAATATCATCACTATGATGATGATGATGATGATGAT 597
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DB 796 CCTCAGATTAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 855
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QY 598 GTTGTCTGATCTGTTGCTTTCAGGCTTTCATCAT 635
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RESULT 4
US-09-023-655-1417
Sequence 1417, Application US/09023655
Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: US/09/023,655
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1417:
SEQUENCE CHARACTERISTICS:
LENGTH: 1973 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9471316
US-09-023-655-1417

Query Match 8.1%; Score 76.4; DB 4; Length 1973;
Best Local Similarity 46.7%; Pred. No. 1.5e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 118 CTGCTGGGTCATTCATTCATTCCTTCTCTGCTGTAAGAAACACCCGTCATGAC 177
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DB 376 CTGGGGAAGTCCCTTGTCATGATGATGATCTCAAGGACACCAAAAGAAAGACGAC 435
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QY 178 ACCATGCGGTCATTAACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
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DB 436 AATATTACATCTTTAACTGCGCCCTGCGGACACTGCTGCTGCTGCTGCTGCTGCT 495
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QY 238 GCTTGACCTTACCTCATCAAGAAAGACTTGATGTTGGCTGCTGCTGCTGCTGCT 297
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DB 496 CAGGACACGACATCTCTGCGCTCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCT 555
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QY 298 AGTGCATGCTGACATCCACATGATGATGATGATGATGATGATGATGATGATGAT 357
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DB 556 ATTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 615
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QY 358 ACCAGATACCTCATCTTCTTCAAGTGCAGAAAGAAAGTGAATCTACAGAAACTGCAT 417
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DB 616 GATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675
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QY 418 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
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DB 676 GCCCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
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QY 478 GTTCTCCCGGTATGAAATCCATGAGAAATGATGATGATGATGATGATGATGATGAT 537
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DB 736 ATCATGGGCTGCGACAGTGCAGAGATGAAGATGAGATGAGATGAGATGAGATGAGAT 795
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QY 538 GAGCTTGCTTACATATGATGAAATATCATCACTATGATGATGATGATGATGATGAT 597
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DB 796 CCTCAGATTAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 855
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 856 CCCGTGCTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5
US-09-976-594-171
Sequence 171, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409

```

? PRIOR FILING DATE: 2000-10-12
? NUMBER OF SEQ ID NOS: 1143
? SOFTWARE: PERL Program
? SEQ ID NO 171
? LENGTH: 3205
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? OTHER INFORMATION: Incyte ID NO. 6673549 222181.1
? US-09-976-594-171

```

Query Match	8.1%;	Score	76.4;	DB 4	Length	3205;
Best Local Similarity	46.7%;	Pred.	No. 2.1e-12;			
Matches 242; Conservative	0;	Mismatches	276;	Indels	0;	Gaps 0;

Qy	118	TTGGGGGATGCAATTTCCATCTTTCTCCGGGAAATGAACCCGGTCAGTAC	177
Db	450	CTGGGGAACTGCCCTTGTCATGTAGCTATCTTCAGGACACCAAAATGAAGACCCACC	509
Qy	178	ACCATGGCGATTAACCTGTGTGTGTGCACAGCGTTTTTCTGTGACAGTGCATTT	237
Db	510	AATATTTTACATCTTTAACTGGCCCTGGCCCAACTGTGTCTGTGACCTGCGCTTC	569
Qy	238	CGCTTGACCTTACCTCATCAAGAACCTGAAAGTTTGGGCGCGCCCTTCGTGAATTTGTG	297
Db	570	CAGGGCAACGACATCTCTCTGGGCTTCTGGCGGTTTGGGAAATGGCTGTGCAAGACATTC	629
Qy	298	AGTGGCATGTGCAACATCCACATGATPACTCAAGTTCCTATTTCTAATGTGTATCCGTGTC	357
Db	630	ATTGCCATGTACTACTACACATGTTTCACGACACCTTCACCCCTAATGCCATGAGTGTG	689
Qy	358	ACCAGATPACCTCATCTTCTTTCAATGACAAAGACAAAGTGAATTTCAAGAAAATGTGAT	417
Db	690	GATGCGTATGTAGCCATCTGCACCCCAATCCGTGCCCTTCGACGTCCGACGTCCAGCAAA	749
Qy	418	GCTGTGGCTGCAGTGTGCTGTGCATGTGACGTGTGATTTGTCATTTGTGTGATCCCTGGTT	477
Db	750	GCCCCAGGCTGTCAATGTGGCCATCTGGGCCCTTGGCTCTGTGTGCGATTTCCGGTGGC	809
Qy	478	GTCTCCCGGTATGCAATTCATGAAGAAATACAAATGAGAGCACTGTTTTAAATTTACAAA	537
Db	810	ATTCATGGGCTGGGACAGGTGCAGAGTGAAGAAATCGAGTCCGTGTGTGAATCCCTTACC	869
Qy	538	GAGCTTGCTTACACATATGTGAAAATCATCAACTATATATAGTCAATTTTGTATAGCC	597
Db	870	CCTCAGAGATTACTGGGGCCCGGTGTGTTTGGCATCTGSCATCTTCTCTTCAATGCTC	929
Qy	598	GTGTCTGTGATTTCTGTGTCTTCCAGGCTTTTCATCAT	635
Db	930	CCCGTGTCTGTATCTCTGTCTGTCTACAGCCTTCATGAT	967

```

RESULT 6
US-09-743-871B-14
: Sequence 14, Application US/09743871B
: Patent No. 6627734
: GENERAL INFORMATION:
: APPLICANT: Memorial Sloan-Kettering Cancer Center
: TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUSE KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
: FILE REFERENCE: 830002-2001..1
: CURRENT APPLICATION NUMBER: US/09/743,871B
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: PCT/US99/15977
: PRIOR FILING DATE: 1997-07-15
: PRIOR APPLICATION NUMBER: 60/093,002
: PRIOR FILING DATE: 1996-07-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 14
: LENGTH: 1134
: TYPE: DNA

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ORGANISM: homo sapiens
US-09-743-871B-14

Query Match	7.8%;	Score 73.2;	DB 4;	Length 1134;
Best Local Similarity	46.8%;	Pred. No. 1e-11;		
Matches 231; Conservative	0;	Mismatches 263;	Indels 0;	Gaps 0

Oy	142	TTCTCTCGGTGAAATGAACACCGGTCAGTACACCATGAGCGGTCACTAACTTGATG	2010
Db	223	TGCTTTGTCAATGACACCAAAATGAAAGACGACCAATATTTCATCTTTAACTGGCC	2828
Oy	202	GTGGTCACAGCGTTTTTTCTGTCACAGTCCATTTTGGCTTGACCTTACCTCATAGAAAG	2615
Db	283	CTGGCCGACACTCTGGTCTCTGTACAGCGTCCCTTCCAGGGACAGACATCTCTTGAGC	3422
Oy	262	ACTTGATGTTTGGGCGTGCCTTTCTGCAGAAATTTGAGATGGCATGTCAGTACATCCATG	3211
Db	343	TTCTGGCCGTTTGGAAATGCGCTGTGCAAGACAGTCATTTGCATTTGACTACTACAACTG	4022
Oy	322	TACCTCACTTCCATTTCTATGTGTGATCCTGGTCAACAGATACCTCATCTTCTTCAAG	3811
Db	403	TTACACAGACCTTCAACCTTACTCCATGAGTGGATCCCTATGTAGCCATCTGCAC	4622
Oy	382	TGCAAGACAAAGTGSAAATTTCACAGAAACATGCATGTGCTGGTCAGTCCGGCATG	4411
Db	463	CCCATCCGTCCTCGACGTCGCCACATTCACAGAAAGCCACGGCTGTCAATGTGGCATTG	5222
Oy	442	TGACGCTGTGATATTGTCAATGTGTACCCCTGTGTGTCTCCGGTATGGAATTCATGAG	5011
Db	523	TGGGCGCTGTCTGTGTGTGTGCGTGTCTCCGTTGCATCATGGGCTCGGACAGGTGAG	5822
Oy	502	GAATACATGAGAGAGACACTGTTTAAATTTACAAAGAGCTTGGTTACACATATGAAA	5611
Db	583	GATGAAGATGACAGGCTCGTGTGAGATCCCTACCCCTCAGAAATACGTGGGCCCCGGTG	6422
Oy	562	ATCATCACTATATGATAGTCAATTTTGTCTATAGCCGTTGCTGTGATTTCTGTGGTCTTC	6211
Db	643	TTTGGCATCTGCAATCTTCTCTTTCCTTCATACGACCCCGATGTGTCATCTGTCTGC	7022
Oy	622	CAGGTCTTCATCAT	635
Db	703	TACAGCTCATGAT	716

```

RESULT 7
US-09-743-871B-13
; Sequence 13, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION: Sloan-Kettering Cancer Center
; APPLICANT: Memorial
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUSE
; TITLE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743,871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093,002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-743-871B-13

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Query Match 7.5%; Score 70.2; DB 4; Length 1177;
 Best Local Similarity 46.6%; Pred. No. 8.8e-11;
 Matches 225; Conservative 0; Mismatches 256; Indels 0; Gaps 0

0y 153 GAAATGACACCCGGTCAGTGACACCAATGCGCGTCTTAACTTGGTGTGTGCACAG 212

QY 153 GAAATGAACACCCGGTCAGTACACACATGGCGGTATTAATTGGTGGTGTCAAG 212

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 72210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 161..1261
US-08-147-592A-5

Query Match 6.4%; Score 59.8; DB 3; Length 1330;
Best Local Similarity 44.8%; Pred. No. 1.4e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

33 CCACATPACTCCAGAAATTCCTTGGCATCTCTATAGTACACCCCATTTATCAGCCT 92
262 CTTCAATGCTAGGCAACGTCCTTCTCCCTTGAGCTCAAGTCAACCATCGTGGGCT 321
93 CTACTCATAGTCTTATTTGGCGGCTGTGTGG--TGTCAATTCATCTTTTCCCT 149
322 CTACTTGGCTGTGTGATCGGGGGGCTCCCGGGAATGCTGTGATGATGATCTCT 381
150 GGTGAAGAATGAACACCCGCTCACTGACACCATGCGCGCTATTAACTTGTGTGTCCA 209
382 CAGGCAACACCAAGATGAAGACTCTACCAATTTACATTTAACTTGGCACTGGCTGA 441
210 CAGCGTTTCTGCTGACATGCGCATTTGCTTGACCTTACCTCATGAAGAAGCTTGAT 269
442 TACCTGGTCTTCTGACACTGCGCTTCCAGGGCACAAGAAATCTTCTGGGCTTGGCC 501
270 GTTTGGGCTCCCTTCTGCAAAATTTGAGTGCATGCTGCACATGCATGTAACCTCAC 329
502 ATTGGGAATGCACTGTGCAAGACGCTATTGCTATGCACTATCAACAATGTTTACAG 561
330 GTTCTATTCTATGTGTGTGATCTGTGTACCAAGATACCTCATCTTCTTCAAGTCAAGA 389
562 CACTTTCATTTGACCTGACATGATGTGAACCGTTATGTATCTTGCCACCTTATCCG 621
390 CAAAGTGAATTTCAAGAAACTGATGCTGTGGCTGCAGTGTGGCATGTGAAGCT 449
622 TGGCTTGATGTTGGAGATCCAGTAAAGCCAGGCGGTTAATGTGGCCATATGGGCGCT 681

450 GGTGATTTGATTTGTGTGATACCCCTGTTGTCTCCCGTATGTGAATTCATGAGAAATACA 509
682 GGCTTCGGTGTGTGTGTGTTCTCTTGCCATATGAGGCTCAGCAAGTGAAGATGAAGA 741
510 TGAGAGCACTGTTTAAATTTACAAAGAGTTGCTTACATATGTGAATAATCATCA 569
742 GATCAGTGCCGTGTGAAGATCCCGCCCTCAGACATAATGGGCGCTGTATTTGCCAT 801
570 CTATATGATGATCATTTTGTGATGACCGTGTGATGATTTGTTGTTCCAGGCTT 629
802 CTGATCTTCTCTTTTCTTCTTCAATCCGGTTGTGATCTCTGTCTGCTACAGCT 861
630 CATCAT 636
862 CATGATT 868

RESULT 10
US-08-292-694A-5
Sequence 5, Application US/08292694A
Patent No. 6319686
GENERAL INFORMATION:
APPLICANT: BELL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUDA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,694A
FILING DATE: August 19, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/147,592
FILING DATE: 5 No. 6319686ember 1993
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US94/05747
FILING DATE: 20 May 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARK B. WILSON
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 161..1261
US-08-292-694A-5

Query Match 6.4%; Score 59.8; DB 3; Length 1330;
Best Local Similarity 44.8%; Pred. No. 1.4e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

```
QY 33 CCACATACCTTCAGAAATTCCTTCGATCCTATAGTACACCCCACTTAATAGCCT 92
DB 262 CCTCATGTGATGACCAAGTGCCTTCCTGCTTGGACTCAAGGTACACCATGTGGGCT 321
QY 93 CTACTTCAATAGTCTTAATTTGGCGGGCTGGTGGG---TGTCAATTCATCTTTTCCTCT 149
DB 322 CTACTTGGCTGTGTGATCGGGGGGCTCCTGGGAATGCCCTGTCATGATGATCATCT 381
QY 150 GGTAAATGAAACACCCGCTAGTACCAACATGGCGGTCAATTAATTTGGTGTGCTCA 209
DB 382 CAGGACACCAAGAAAGACTGTACCAATTTCAATTTAATTTGGCACTGGCTGA 441
QY 210 CAGCGTTTTCGTGACAGTGGCATTTGGCTTGAACCTCATCAAGAAAGACTTGGAT 269
DB 442 TACCTGTCTTGTGACACTGCTTCAGGGGCAAGACATCTTCTGGGCTTCTGGCC 501
QY 270 GTTGGGCTGCTTCGCAATTTGTGAGTGCATGTCGACATCCATGATACCTGAC 329
DB 502 ATTGGGAATGACATGTGCAAGAGCGTCAATGTCAATGACATCAATGATTTTACGAG 561
QY 330 GTTCCATTTATGTGTGTGATCTGTGTCACAGATACCTCATCTTTCAAGTGCMAAGA 389
DB 562 CACTTCACTTGAAGTGCATGATGATGAGCGTTATATGATCTCCACCCATATCG 621
QY 390 CAAGTGAATTTACAGAAATGCAAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 449
DB 622 TGCCTGTGATTTGGACATCAAGTAAAGCCAGGCGTTAATGTGGCATATGGGCTT 681
QY 450 GGTGATGTCAATGTGTGATCCCTGTGTGTCTCCGCGATGAAATCCATGAGAAATACA 509
DB 682 GGTTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 741
QY 510 TGAGAGACATGTTTAAATTTCAAAAGACTGTGCTTACATATGTGAAATCATCA 569
DB 742 GATGAGTGTGTGTGATGATCCCGCCCTCAGGACATATGGGGCCCTGATTTGGCAT 801
QY 570 CTATATGATGATTTTGTGATAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 629
DB 802 CTGACATCTTCTTTTTCCTTATCATCCCGTTCTGATCATCTGTGTGTGTGTGTGT 861
QY 630 CATCAT 636
DB 862 CATCAT 868
```

RESULT 11

US-08-889-108-16
Sequence 16, Application US/0889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/305,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

SEQUENCE CHARACTERISTICS:

LENGTH: 1567 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 173..1273

US-08-889-108-16

Query Match 6.4%; Score 59.8; DB 3; Length 1567;
Best Local Similarity 45.6%; Pred. No. 1.5e-07;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

```
QY 89 GCCTCTCATGATGAGTATTTGGCGGGCTGGTGGG---TGTCAATTCATCTTTTCC 145
DB 330 GGTCTCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 389
QY 146 TCCGTGAAATGAAACACCCGCTGATGACCAACATGCGGTCAATTAATTTGGTGTG 205
DB 390 TCCGACAGACACCAAGATGAAGACATGACCAATTTAATTTATGTGCACTGG 449
QY 206 TCCACAGCTTTTCTGTGACAGTGCATTTGCTTGCCTTACCTCATCAAGAACTT 265
DB 450 CTGATACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 509
QY 266 GAGTGTGTGCTGCTTCTGCAATTTGTGATGTCATGTCGACATCATGATGATGAC 325
DB 510 GGCATTTGGGAATGACCTGTGCAAGACTGTGATGATGATGATGATGATGATGAT 569
QY 326 TCACTTCTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 385
DB 570 CCAGACTTTTATCTGTACCGCATGAGCGTATGAGCGTATGATGATGATGATGAT 629
QY 386 AAGACAAAGTGAATTTACAGAAATGCAAGTGTGCTGTGCAAGTGTGCAATGTGA 445
DB 630 TCCGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689
QY 446 CGCTGTGATTTGATTTGTGTGATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 505
DB 690 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
QY 506 ACAATGAGACATGTTTAAATTTCAAAAGACTGTGCTTACATATGTAAGAAATCA 565
DB 750 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 809
QY 566 TCACTATATGATGATGATTTTGTGATAGCGGTGTGATGATGATGATGATGATGAT 625
DB 810 CCATGTGATCTTCTTTTTCCTTATCATCCCGTGTGATGATGATGATGATGATGAT 869
QY 626 TCTTCATCAT 636
DB 870 GCCTCATGAT 880
```

RESULT 12

PCT-US94-10358-16
Sequence 16, Application PC/TUS9410358

GENERAL INFORMATION:
APPLICANT: NI OPIOID RECEPTORS: COMPOSITIONS AND METHODS
TITLE OF INVENTION: 17
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: IND005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
PCT-US94-10358-16

Query Match 6.4%; Score 59.8; DB 5; Length 1567;
Best Local Similarity 45.6%; Pred. No. 1.5e-07;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

89 GCCTCTACTTCAATGCTTATTTGGCGGCTGTGGG---TGTCATTTCCATTTCTTTCC 145
Db 330 GGCCTACTTGGCTGTGTGATGGGGGGCTCCCTGGGAACTGCTGTATGATGCA 389
QY 146 TCCTGTGAAATGAACAACCCGGTCACTGACCAACCATGGCGGTCATTAACTGGTGTGG 205
Db 390 TCCTCAAGGACACCAATGAAGACAGTACCAATTTACATTTAATCTGGACACTGG 449
QY 206 TCACAAGGTTTTCTGTGACATGGCATTTGGCTTGACCTACTTCAATGAAGAAGCTT 265
Db 450 CTGTATACCTGTGTCTTGTCACTGCTTCCAGGACAGACATCTTACCTGGGCTTCT 509
QY 266 GGAATTTGGGCTCCCTTCTGCAAAATTTGAGTGCATGCTGCATCCACATGTAC 325
Db 510 GGCATTTGGGAATGCACTCTGCAAGACTGTGATTTGATGACTTACAACTGTGTTA 569
QY 326 TCAGCTCTATTCTATGTGTGTATCTGTGTACCAAGTATCTCATCTTTCAAGTGA 385
Db 570 CCACACCTTTTACTGTACCGCATGAGCGTACCGCTATGTGGTATCTGCCACCTTA 629
QY 386 AAGCAAGTGAATTTCAAGAAATGCAATGCTGTGGCTGCCAGTGTGGCATGTGGA 445
Db 630 TCCGTGCCCTTGAATGTGCAATCCAGCAAGGCCAGGCTGTAAATGTGGCCATATGGG 689
QY 446 CGCTGTGATTTGATTTGTGTGTTACCCCTGTGTGTCTCCGGTATGGAATCATGAGGAAT 505

Db 690 CCCTGGCTCAGTGTGTGTGTTCTGTGGCATCATGGGTTCCAGCAAGTGAAGATG 749
QY 506 ACATATGAGAGACTGTTTAAATTTACAAAAGCTTGTCTTACATATGTGAATAATCA 555
Db 750 AAGATATGAGTGTGTGTGAGATCCGCCCTAGAGACTATTTGGGGCCCTGTATTTG 809
QY 566 TCACTATATGATGATGATTTTGTGATGACCGGTGCTGTGATTTCTGTTGTTCCAGG 625
Db 810 CCATCTGATCTTCTTTTCTTCTTCTTATCATCCCTGTGTGATCATCTGTCTGATCA 869
QY 626 TCTTCATCATTT 636
Db 870 GCCTCATGATT 880

RESULT 13
US-08-986-209A-1
Sequence 1, Application US/08986209A
Patent No. 6660496
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
APPLICANT: Pasternak, Gavril W
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTOR
TITLE OF INVENTION: THEREBY, AND USES THEREOF
FILE REFERENCE: 830002-2004
CURRENT APPLICATION NUMBER: US/08/986,209A
CURRENT FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2600
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (299)..(1402)
OTHER INFORMATION:
US-08-986-209A-1

Query Match 6.4%; Score 59.8; DB 4; Length 2600;
Best Local Similarity 44.8%; Pred. No. 2.1e-07;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

33 CCACATATCTCCAGGAATTCCTTGTGCATCTCTATATGACACCCCATTTATTCAGCTT 92
Db 400 CTTCAATGTGAGCAAGTGCCTTCTGCCCCCTTGAATCAAGTACCAATCGTGGGCT 459
QY 93 CTACTTCAATGATGCTTATTTGGCGGCTGTGGG---TGTCATTTCCATTTCTTCTCT 149
Db 460 CTACTTGGCTGTGTGATCGGGGGGCTCTGGGAACTGCTGTATGATGATCTTCT 519
QY 150 GGTGAAATGAAACCCCGTCACTGACCAACATGGCGGTCAATTAATCTGTGTGTGCA 209
Db 520 CAGGACACCAAGATGAAGCTGTACCAATTTACATTTAATCTGGCACTGGCTGA 579
QY 210 CAGCGTTTTCTGTGACATGTCATTTGCTTGAATCTTCAATCAAGAAGCTTGAT 269
Db 580 TACCTGTGTCTGTGACCTGCTTCCAGGACAGACATCTTCTGGGCTTCTGGCC 639
QY 270 GTTTGGGCTCCCTTCTGCAAAATTTGAGTGCATGCTGCATCCACATGATACCTCAC 329
Db 640 ATTTGGGAATGACCTGTGCAAGCGGCTATGTCTATGTGACTTACAACTGTTTACAG 659
QY 330 GTTCTATTCTATGTGTGTATCTGTGTACCAAGTATCTCATCTTTCAAGTGA 389
Db 700 CACTTCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
QY 390 CAAAGTGAATTTCAAGAAATGCAATGCTGTGGCTGCCAGTGTGGCATGTGAGACT 449
Db 760 TGCCCTTGTATGTGTGATCCAGTAAAGGCCAGGCGGTTAAATGTGGCCATATGGGCGCT 819
QY 450 GGTGATTTGATTTGTGTGTATCCCTGTGTGTCTCCGGTATGGAATCATGAGGAATCA 509

Db 820 GGCCTCGGTGTTGGTGTCTCTGTCATATGGGCTCAGACCAAGTGGAGTGAAGA 879
Qy 510 TGAGAGACATGTTTAAATTTCAACAAAGCTGCTTACATATGTGAATAATCAACA 569
Db 880 GATCGAGTGGCTGGTGGAGATCCCGCCCTCAGGACTATTGGGGCCCTGTATTGGCAT 939
Qy 570 CTATATGATGATCAATTTTGTGCATAGCGGTGCTGTATCTTGTGTGCTTCCAGTCTT 629
Db 940 CTGATCTTCTCTTTTCTCTTCATCATCCGCTTGTATCATCTCTGTCTCTACAGCT 999
Qy 630 CATCAT 636
Db 1000 CATGATT 1006

RESULT 14

US-08-454-549-1
Sequence 1, Application US/08454549
Patent No. 5866324
GENERAL INFORMATION:
APPLICANT: EPPLE, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HUMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: NO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
TISSUE TYPE: Rat brain
US-08-454-549-1

Query Match 6.4%; Score 59.8; DB 2; Length 2706;
Best Local Similarity 45.6%; Pred. No. 2.1e-07;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
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Db 264 GGCTCTACTGCTGTGTGTCATCGGGGGCTCCCTGGGAACTGCTGTATGTATGTCA 323
Qy 146 TCCGTGTGAATAATGACACCCGCTCAGTGAACACCATGGCGGTCAATTAACCTGGTGG 205
Db 324 TCCCTACAGGACACCAAGATGAAGACAGCTACCAACATTTTACATTTTAATCTGCACTGG 383

Qy 206 TCCACAGCTTTTCTCTGACAGTCCATTTGCTTACCTTACATCAAGAAGACTT 265
Db 384 CTGATACCTGCTCTCTTAACACTGCTTCCAGGGCAGACAGATCTTACTGGGCTTCT 443
Qy 266 GGATGTTGGGCTGCCCTTCTGCAAAATTGTGAGTGCATAGCTGCACATCCAGATGACC 325
Db 444 GGCCATTGGGAATGACCTTGCAGAGCTGTCAATGCTATATGACTACTTACCAACATGTTA 503
Qy 326 TCAAGTCTCAATTTATGATGATGATCCCTGCTACAGATATCTCATCTTCTTCAAGTGA 385
Db 504 CCAAGCACTTTTACTCTGACCGGCATAGCGCTAAGCCGTATGTCATCTGCACACCTTA 563
Qy 386 AAGACAAAGTGAATTTCTACAGAAACTGATGCTGTGCTGCAGTGTGGCAATGTGA 445
Db 564 TCCGTGCCCTTGATGTGCGACATCCAGCAAGCCAGGCTGTAAATGTGGCCATATGGG 623
Qy 446 CGCTGGATTTGATGATGATGATCCCTGCTGTCTCCGCTATGAAATCATAGAGGAAT 505
Db 624 CCTGGCTTGAAGTGTGTGTCTGTCTGTCTGTCATATGAGTTTACAGCAAGAGTGAATG 683
Qy 506 ACAATGAGAGCACTGTTTAAATTTCAACAAAGCTTGTCTTACATATGTGAATAATCA 565
Db 684 AAGAGATGAGTGTCTGTGGAATCCCTGCCCTAGAGCTATGGGGCCCTGTATTCG 743
Qy 566 TCACTATATGATGATTTTGTCTATGACCCGCTGTGATTTCTGTGCTTCCAGG 625
Db 744 CCACTGCACTTCTCTTTTCTCTTCAATCCCTGTGATCATCTGTCTGTCTACA 803
Qy 626 TCTTTCATCAT 636
Db 804 GCCTCATGATT 814

RESULT 15

US-08-454-552-1
Sequence 1, Application US/08454552
Patent No. 6005072
GENERAL INFORMATION:
APPLICANT: EPPLE, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HUMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: NO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,552
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
 ;
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: cDNA
 ;
 ; ORIGINAL SOURCE:
 ;
 ; TISSUE TYPE: Rat brain
 ;
 ; US-08-454-552-1

Query Match 6.4%; Score 59.8; DB 3; Length 2706;
 Best Local Similarity 45.6%; Pred. No. 2.1e-07;
 Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

QY 89 GCCCTACTTCATATGCTTATTGCGGGCTGGTGG--TGTCAATTCATTCCTTTCC 145
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 Db 264 GGCCTACTTGGCTGTGTCATCGGGGGCTCCGTGGGAACCTGCTGTATGATGTCA 323
 QY 146 TCCGTGTAATAAGAACCCGGTCACTGACACCATGGCGGTCAATTAATTGGTGTGG 205
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 Db 324 TCCCTAGGACACCAAGATGAGACAGCTACCAATTACATATTTAATCTGGCACTGG 383
 QY 206 TCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGAACCTACCTCATCAAGAACTT 265
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 Db 384 CTGATACCTGTGCTTGTACACTGCCCTTCCAGGGCACAGACATCTACTGGCTTCT 443
 QY 266 GGATGTTGGGCTGCCCTTCTGCAATTGTGAGTGCATGTGCACATCCACATGTACC 325
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 Db 444 GGGCATTTGGGAATGCACTGTGCAAGACTGTCAATGTCTATGACTACATCATGTTTA 503
 QY 326 TCAAGTTCCTATTCTATGTGTGATCTGTGTCACAGATACCTCATCTTCTTCAAGTGA 385
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 Db 504 CCAGCACTTTTACTCTGACCGCCCATGAGCGTACACCGTATGTGGCTATCTGCCACCTTA 563
 QY 386 AAGACAAAGTGAATTCTACAGAAACTGCATGCTGTGGCTGCAAGTGTGCATGTGA 445
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 Db 564 TCCGTGCCCTTGAATGTCGACATCCAGCAAGCCAGGCTGTTAATGTGGCCATATGGG 623
 QY 446 CGCTGTGATTTGATTTGTAACCCCTGTGTGTCTCCCGTATGGAATCATGAGGAAT 505
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 Db 624 CCGTGGCTTCAAGTGTGTGTTCTGTGTGTCATCATGGGTTCAAGCAAGTGGGAAGATG 683
 QY 506 ACAATGAGAGCACTGTTTAAATTTCACAAAGAGCTTGCTTACATATGTGAAATCA 565
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 Db 684 AAGAGATCGAGTGTGTGAGAGATCCCTGCCAGACTATTTGGGGCCCTGTATTCG 743
 QY 566 TCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTGTGTCTTCCAGG 625
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 Db 744 CCAATCTGCAATCTTCTTTTCTTCTTCAATCCCTGTGTGATCATCTGTGTCTGTACA 803
 QY 626 TCTTCATCATTT 636
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 Db 804 GCCTCATGATT 814

Search completed: September 9, 2005, 22:50:16
 Job time : 172.402 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 22:41:45 ; Search time 677.311 Seconds
(without alignments)
9104.583 Million cell updates/sec

Title: US-10-085-233B-3

Perfect score: 939
Sequence: 1 atgcaaaaatgtactctcc.....ggaaatgtgttctgtgcgcg 939

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/1/pubpna/PCF_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
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- 9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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- 16: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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- 20: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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- 23: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*
- 24: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	939	100.0	14	US-10-085-233B-3	Sequence 3, Appli
2	939	100.0	14	US-10-085-233B-1	Sequence 1, Appli
3	937.4	99.8	1336	US-10-467-252-52	Sequence 52, Appli
4	928.2	98.8	1340	US-10-467-252-53	Sequence 53, Appli
5	928.2	98.8	1460	US-10-467-252-54	Sequence 54, Appli
6	928.2	98.8	2525	US-09-782-974C-81	Sequence 81, Appli
7	928.2	98.8	2525	US-10-467-492A-81	Sequence 81, Appli

8	928.2	98.8	2525	21	US-10-975-979-81	Sequence 81, Appli
9	927.8	98.8	1318	15	US-10-017-161-1193	Sequence 1193, Ap
10	927.8	98.8	113306	17	US-10-292-798-1007	Sequence 1007, Ap
11	913.4	97.3	918	9	US-09-995-225-3	Sequence 3, Appli
12	913.4	97.3	918	10	US-09-995-225-3	Sequence 3, Appli
13	913.4	97.3	918	14	US-10-055-106C-1	Sequence 1, Appli
14	913.4	97.3	918	14	US-10-188-405-9	Sequence 9, Appli
15	913.4	97.3	918	17	US-10-297-908A-2	Sequence 2, Appli
16	913.4	97.3	1040	15	US-10-293-171-1	Sequence 1, Appli
17	913.4	97.3	1632	21	US-10-505-488-212	Sequence 212, App
18	907.4	96.6	1499	19	US-10-398-036-22	Sequence 22, Appli
19	559.2	59.6	810	16	US-10-366-504-1	Sequence 1, Appli
20	404.4	43.1	447	10	US-09-782-974C-21	Sequence 21, Appli
21	404.4	43.1	447	21	US-10-467-492A-21	Sequence 21, Appli
22	404.4	43.1	447	21	US-10-975-979-21	Sequence 21, Appli
23	83.6	8.9	600	22	US-10-972-079-57479	Sequence 57479, A
24	76.4	8.1	1113	10	US-09-826-509-540	Sequence 540, App
25	76.4	8.1	1113	21	US-10-925-095-540	Sequence 540, App
26	76.4	8.1	1805	9	US-09-823-114-18	Sequence 18, Appli
27	76.4	8.1	1805	15	US-10-290-748-18	Sequence 18, Appli
28	76.4	8.1	1829	10	US-09-905-186A-9	Sequence 9, Appli
29	76.4	8.1	1829	10	US-09-905-186A-10	Sequence 10, Appli
30	76.4	8.1	1829	10	US-09-905-186A-11	Sequence 11, Appli
31	76.4	8.1	1973	17	US-10-305-720-1391	Sequence 1391, Ap
32	76.4	8.1	1973	18	US-10-641-643-1417	Sequence 1417, Ap
33	76.4	8.1	1973	22	US-10-498-848-1	Sequence 1, Appli
34	76.4	8.1	2534	14	US-10-087-345A-22	Sequence 22, Appli
35	76.4	8.1	2534	15	US-10-225-567A-208	Sequence 208, App
36	76.4	8.1	2534	17	US-10-352-684A-31	Sequence 31, Appli
37	76.4	8.1	2534	21	US-10-753-267-77	Sequence 77, Appli
38	76.4	8.1	2534	22	US-10-848-637-22	Sequence 22, Appli
39	76.4	8.1	2534	24	US-11-011-450-22	Sequence 22, Appli
40	76.4	8.1	3330	20	US-10-723-860-7345	Sequence 7345, Ap
41	74.8	8.0	1829	10	US-09-905-186A-7	Sequence 7, Appli
42	74.8	8.0	1829	10	US-09-905-186A-8	Sequence 8, Appli
43	73.2	7.8	1134	19	US-10-606-592-14	Sequence 14, Appli
44	71.6	7.6	110218	13	US-10-087-192-1345	Sequence 1345, Ap
45	70.4	7.5	593	16	US-10-029-386-9800	Sequence 9800, Ap

ALIGNMENTS

RESULT 1
US-10-085-233B-3
; Sequence 3, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLICKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; FILE REFERENCE: RECEPTOR AND USBS THEREFOR
; CURRENT APPLICATION NUMBER: US/10/085,233B
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(939)
US-10-085-233B-3

Query Match 100.0%; Score 939, DB 14; Length 939;
Best Local Similarity 100.0%; Pred. No. 9.9e-271;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61	GATCCTATAGTACACCCCACTTAATCAGCTCTTACTTCAATAGTGTATATGGCGGGCTG	120
Qy	121	GTGGGTGTCATTTCCATTCTTTTCTCTGGTGAATAATGACACCCGGTCAATGACACC	180
Db	121	GTGGGTGTCATTTCCATTCTTTTCTCTGGTGAATAATGACACCCGGTCAATGACACC	180
Qy	181	ATGGGGGTCAATTAACCTGGTGGGGCCACAGGTTTTCTGTGACAGTGCATTTGCG	240
Db	181	ATGGGGGTCAATTAACCTGGTGGGGCCACAGGTTTTCTGTGACAGTGCATTTGCG	240
Qy	241	TTGACCTTACCTCATGAAGAAGCTTGGAATGTTGGGCTGCCCTTCGCAAAATTTGAGT	300
Db	241	TTGACCTTACCTCATGAAGAAGCTTGGAATGTTGGGCTGCCCTTCGCAAAATTTGAGT	300
Qy	301	GCCATGCTGACATCCACATGTACTCAGGTTCTATTTCTATGTGTATCCTGTGCACC	360
Db	301	GCCATGCTGACATCCACATGTACTCAGGTTCTATTTCTATGTGTATCCTGTGCACC	360
Qy	361	AGATACCTCATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCTACAGAAACCTGCATGCT	420
Db	361	AGATACCTCATCTTCTTCAAGTGAAGCAAGCAAGTGAATTTCTACAGAAACCTGCATGCT	420
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Qy	481	TCCCGTATGGAATCCATGAGAAATACAAATGAGAGCACTGTTTAAATTTCAAAAAG	540
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Qy	541	CTTGCTTACATATGTGAAATACATCACTATATATGTGCTATTTTGTGCATAGCCGT	600
Db	541	CTTGCTTACATATGTGAAATACATCACTATATATGTGCTATTTTGTGCATAGCCGT	600
Qy	601	GCTGTGATTTCTTGGTCTTCAGAGCTTCATCATATGTGATGTGAGAGCTACGC	660
Db	601	GCTGTGATTTCTTGGTCTTCAGAGCTTCATCATATGTGATGTGAGAGCTACGC	660
Qy	661	CACCTCTTAATCCACAGAGGTTCTGGGCTCAGCTGAAAAACCTATTTTATATAGG	720
Db	661	CACCTCTTAATCCACAGAGGTTCTGGGCTCAGCTGAAAAACCTATTTTATATAGG	720
Qy	721	GTTCATCCTGTTGTTTCTTCCCTACAGATCTTATAGATCTATTAATCTTGAATGTTG	780
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Qy	781	ACGCATTCGAATGCCGTGAGACAGAGTGTGATTTATACGAATCTTCTGAGGTGA	840
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Qy	841	ACAGCAATTAGCTGCTATGATTTGCTCTCTTGTCTTTGGGGGAAGCCATTGGTTAAG	900
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RESULT 2
US-10-08

Sequence 1, Application US/10085233B
Publication No. US20030087249A1
GENERAL INFORMATION:
APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
RECEPTOR AND USES THEREFOR
TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
FILE REFERENCE: MP/2001-021P/NCPTM
CURRENT APPLICATION NUMBER: US:10/085,233B

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? CURRENT FILING DATE: 2002-02-28
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? PRIOR APPLICATION NUMBER: 60/272,677
? PRIOR FILING DATE: 2001-03-01
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
?
? LENGTH: 1684
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
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? FEATURE:
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? NAME/KEY: CDS
? LOCATION: (147)...(1085)
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Query Match	100.0%;	Score 939;	DB 14;	Length 1684;
Best Local Similarity	100.0%;	Pred. No. 1.4e-270;		
Matches 939;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	207	GATCCATATAGGACACCCCACTTAATCAGCCCTTA	CTCAATGATCTTAATTTGGCGGCGT	266
OY	121	GTGGGTGCATTTTCCATTTCTTTCTCTGTGAAAATGA	CAACCCGGTCAGTGACACCC	180
Db	267	GTGGGTGCATTTTCCATTTCTTTCTCTGTGAAAATGA	CAACCCGGTCAGTGACACCC	326
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Db	807	CACCTTTTACATATCCACACAGAGATTCTGGGCTCA	CGCTGAAAACCTATTTTTTATAGGG	866
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US-10-467-252-52
; Sequence 52. Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HAFALIA, April J.A.; RAMKOMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y. Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dying Aina M.;
; APPLICANT: GRAU, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junming;
; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,332;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 52
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 90012430CB1
US-10-467-252-52

Query Match 99.8%; Score 937.4; DB 19; Length 1336;
Best Local Similarity 99.9%; Pred. No. 3,7e-270;
Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCAAAAATGTGACTTCCCAAGATGCTGTGGCAATACCTCCAGAAATCTCTTGC 60
Db 195 ATGCAAAAATGTGACTTCCCAAGATGCTGTGGCAATACCTCCAGAAATCTCTTGC 254
Qy 61 GATCTTATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTGTATTTGGCGGCTG 120
Db 255 GATCTTATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTGTATTTGGCGGCTG 314

Qy 121 GTGGGTGTCATTTTCATTTCTTTCTCTGTGTGAAATGAACACCCGGTCAATGACACC 180
Db 315 GTGGGTGTCATTTTCATTTCTTTCTCTGTGTGAAATGAACACCCGGTCAATGACACC 374
Qy 181 ATGGCGGTCAATTAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 375 ATGGCGGTCAATTAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 434
Qy 241 TTGACCTTACTTCAATGAAGACTTTGGATTTTGGGCTGCTTGTCAATTTTGTGAGT 300
Db 435 TTGACCTTACTTCAATGAAGACTTTGGATTTTGGGCTGCTTGTCAATTTTGTGAGT 494
Qy 301 GCCATGTGCAATTCACATGTAACCTCAGTCTCTTCAATGATGATGATGATGATGATGATG 360
Db 495 GCCATGTGCAATTCACATGTAACCTCAGTCTCTTCAATGATGATGATGATGATGATGATG 554
Qy 361 AGATACCTCATCTTCTTCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
Db 555 AGATACCTCATCTTCTTCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 614
Qy 421 GTGGCTGCAAGT 480
Db 615 GTGGCTGCAAGT 674
Qy 481 TCCCGGATAGGAATTCATGAGGAATCAATGAGAGACGTTTAAATTTCAAAAGAG 540
Db 675 TCCCGGATAGGAATTCATGAGGAATCAATGAGAGACGTTTAAATTTCAAAAGAG 734
Qy 541 CTGTCTTACATATGATGAAATCATCACTATATAGTAGTCAATTTTGTCAATAGCGGT 600
Db 735 CTGTCTTACATATGATGAAATCATCACTATATAGTAGTCAATTTTGTCAATAGCGGT 794
Qy 601 GCTGTGATTTGT 660
Db 795 GCTGTGATTTGT 854
Qy 661 CACTCTTCTATCCCAACAGAGGCTGTGGGCTCACTGAAACCAATTTTATATAGG 720
Db 855 CACTCTTCTATCCCAACAGAGGCTGTGGGCTCACTGAAACCAATTTTATATAGG 914
Qy 721 GTCATCTTGT 780
Db 915 GTCATCTTGT 974
Qy 781 ACGCATTCAGATGCTGTAGACAGCAAGGTGCAATTTATACGAAATCTTCTGAGTGA 840
Db 975 ACGCATTCAGATGCTGTAGACAGCAAGGTGCAATTTATACGAAATCTTCTGAGTGA 1034
Qy 841 ACGCAATTAAGCTGTATGATTTGCTTCTTCTTTGGGGGAAGCAATTTGTTAAG 900
Db 1035 ACGCAATTAAGCTGTATGATTTGCTTCTTCTTTGGGGGAAGCAATTTGTTAAG 1094
Qy 901 CAAAAGATAATGGCTTATGGAATTTGTTTGTGCGGT 939
Db 1095 CAAAAGATAATGGCTTATGGAATTTGTTTGTGCGGT 1133

RESULT 4
US-10-467-252-53
; Sequence 53. Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HAFALIA, April J.A.; RAMKOMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y. Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BURFORD, Neil; LU, Dying Aina M.;
; APPLICANT: GRAU, Richard C.; KAHN, Farrah A.;

```

1  APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
2  APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
3  APPLICANT: WARREN, Bridget A.; YANG, Junming;
4  APPLICANT: LEE, Ernestine A.; HARLAND, Jee
5  TITLE OF INVENTION: G-PROTEIN COUPLER RECEPTORS
6  FILE REFERENCE: PI-0357 USN
7  CURRENT APPLICATION NUMBER: US/10/467,252
8  CURRENT FILING DATE: 2003-08-06
9  PRIOR APPLICATION NUMBER: PCT/US02/03635
10 PRIOR FILING DATE: 2002-02-06
11 PRIOR APPLICATION NUMBER: US 60/267,322;
12 PRIOR FILING DATE: 2001-02-07
13 PRIOR APPLICATION NUMBER: US 60/271,215
14 PRIOR FILING DATE: 2001-02-23
15 PRIOR APPLICATION NUMBER: US 60/274,551
16 PRIOR FILING DATE: 2001-03-08
17 PRIOR APPLICATION NUMBER: US 60/278,507
18 PRIOR FILING DATE: 2001-03-23
19 PRIOR APPLICATION NUMBER: US 60/280,597
20 PRIOR FILING DATE: 2001-03-30
21 PRIOR APPLICATION NUMBER: US 60/281,107
22 PRIOR FILING DATE: 2001-04-02
23 PRIOR APPLICATION NUMBER: US 60/282,121
24 PRIOR FILING DATE: 2001-04-06
25 NUMBER OF SEQ ID NOS: 96
26 SOFTWARE: PERL Program
27 SEQ ID NO 53
28 LENGTH: 1340
29 TYPE: DNA
30 ORGANISM: Homo sapiens
31 FEATURE:
32 NAME/KEY: misc_feature
33 OTHER INFORMATION: Incyte ID No: 90012586CB1
34 US-10-467-252-53

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Db	685	TATGAAATCCATNGAGAAATACATGAGGAGCACTGTTTAAATTCCAAAGAGCTTGCT	744
OY	547	TACACATATGTGAAAATATATCACTATATGATAGTACATTTTGTGATAGCCGTGCTGCG	606
Db	745	TACACATATGTGAAAATATCATCACTATATGATAGTACATTTTGTGATAGCCGTGCTGCG	804
OY	607	ATTCTGTGGTCTTCCAGGTCTTTCATCATATGATGATGTCGACAACTACGCCACTCT	666
Db	805	ATTCTGTGGTCTTCCAGGTCTTTCATCATATGATGATGTCGACAACTACGCCACTCT	864
OY	667	TTACTATCCACACAGAGTCTGCGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTATC	726
Db	865	TTACTATCCACACAGAGTCTGCGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTATC	924
OY	727	CTGTGTTGTTCCCTCCCTACAGTCTTTAGAGATCTATCTGAAATGTTGTAGCGCAT	786
Db	925	CTGTGTTGTTCCCTCCCTACAGTCTTTAGAGATCTATCTGAAATGTTGTAGCGCAT	984
OY	787	TCCAAATGCTGTAGCAGACAAAGTTCATTTTATAAGAAATCTTCTTGAGTGTAAACAGA	846
Db	985	TCCAAATGCTGTAGCAGACAAAGTTCATTTTATAAGAAATCTTCTTGAGTGTAAACAGA	1044
OY	847	ATTAGCTGTATGATTTGCTTCTCTTGTCTTTGGGGAGACCAATGGTTTAAAGCAAAAG	906
Db	1045	ATTAGCTGTATGATTTGCTTCTCTTGTCTTTGGGGAGACCAATGGTTTAAAGCAAAAG	1104
OY	907	ATAATATGCTATAGGAATTTGTGTTTGTGGCCGT	939
Db	1105	ATAATATGCTATAGGAATTTGTGTTTGTGGCCGT	1137

LENGTH: 1460
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 90012670CB1
US-10-467-252-54

Query Match 98.8%; Score 928.2; DB 19; Length 1460;
Best Local Similarity 99.7%; Pred. No. 2.3e-267;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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7 AAATGAGCTTCCCAAGATGCTGGGCAACATCTCCAGGAATTCCTTGGAATCCT 66
325 ACAGGTACTTCCCAAGATGCTGGGCAACATCTCCAGGAATTCCTTGGAATCCT 384
67 ATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTCTTATTTGGCGGTGGT 126
385 ATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTCTTATTTGGCGGTGGT 444
127 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 186
445 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 504
187 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 246
505 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 564
247 TACCTCATCAAGAAAGACTTGATGTTGGGCTGCTTCAATTTGAGTGCCATG 306
565 TACCTCATCAAGAAAGACTTGATGTTGGGCTGCTTCAATTTGAGTGCCATG 624
307 CTGCAATTCATCAATGATCACTTCACTTCTTATTTATTTGATGCTGTCACCAAT 366
625 CTGCAATTCATCAATGATCACTTCACTTCTTATTTATTTGATGCTGTCACCAAT 684
367 CTCAATTCATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 426
685 CTCAATTCATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 744
427 GCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
745 GCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
487 TATGGAATTCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGACTTGT 546
805 TATGGAATTCATGAGAAATCAATGAGAGACATGTTTAAATTTCAAAAGACTTGT 864
547 TACCAATGATGAAATCAATCAATATATATATATATATATATATATATATATATAT 606
865 TACCAATGATGAAATCAATCAATATATATATATATATATATATATATATATATAT 924
607 ATTCTGTGTGCTTCCAGTCTTCAATATATATATATATATATATATATATATATAT 666
925 ATTCTGTGTGCTTCCAGTCTTCAATATATATATATATATATATATATATATATAT 984
667 TTAATATCCACCAAGAGTCTGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 726
985 TTAATATCCACCAAGAGTCTGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1044
727 CTGTTGTGTGCTTCCAGTCTTCAATATATATATATATATATATATATATATATAT 786
1045 CTGTTGTGTGCTTCCAGTCTTCAATATATATATATATATATATATATATATATAT 1104
787 TCCAAATGCTGTAGCAAGAGTGTGATTTTATTAACAAATCTTCTGAGGTAAACGA 846
1105 TCCAAATGCTGTAGCAAGAGTGTGATTTTATTAACAAATCTTCTGAGGTAAACGA 1164
847 ATTAGCTGTATGATTTGCTTCTTCTTGTGTTGGGGAAAGCAATGTTTAAAGCAAG 906
1165 ATTAGCTGTATGATTTGCTTCTTCTTGTGTTGGGGAAAGCAATGTTTAAAGCAAG 1224
907 ATTAGCTGTATGATTTGCTTCTTCTTGTGTTGGGG 939
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Db 1225 ATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTCTTATTTGGCGGTGGT 1257

RESULT 6
US-09-782-974C-81
Sequence 81: Application US/09782974C
Publication No. US20030082534A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Lind, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OR INVENTION: No. US20030082534A1 G Protein Coupled Receptor
FILE REFERENCE: 411USPHRM311
CURRENT APPLICATION NUMBER: US/09/782,974C
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/714,449
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 2525
TYPE: DNA
ORGANISM: Homo sapiens
US-09-782-974C-81

Query Match 98.8%; Score 928.2; DB 10; Length 2525;
Best Local Similarity 99.7%; Pred. No. 3.2e-267;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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7 AAATGAGCTTCCCAAGATGCTGGGCAACATCTCCAGGAATTCCTTGGAATCCT 66
9 ACAGGTACTTCCCAAGATGCTGGGCAACATCTCCAGGAATTCCTTGGAATCCT 68
67 ATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTCTTATTTGGCGGTGGT 126
69 ATAGTGAACCCCACTTAATAGGCTTACTTCAATAGTCTTATTTGGCGGTGGT 128
127 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 186
129 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 188
187 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 246
189 GTCAATTCATTTCTTCTCTCTGTGAAAATGAACCCGGTCAATGACCAATGGCG 248
247 TACCTCATCAAGAAAGACTTGATGTTGGGCTGCTTCAATTTGAGTGCCATG 306
249 TACCTCATCAAGAAAGACTTGATGTTGGGCTGCTTCAATTTGAGTGCCATG 308
307 CTGCAATTCATCAATGATCACTTCACTTCTTATTTATTTGATGCTGTCACCAAT 366
309 CTGCAATTCATCAATGATCACTTCACTTCTTATTTATTTGATGCTGTCACCAAT 368
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QY 367 CTCATCTTCTTCAAGTCAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGGGCT 426
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Db 369 CTCATCTTCTTCAAGTCAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGGGCT 428
| | | | |
QY 427 GCCAGTCTGGCAGATGAGACGCTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCG 486
| | | | |
Db 429 GCCAGTCTGGCAGATGAGACGCTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCG 488
| | | | |
QY 487 TATGGAATCCATAGGAATACATGAGAGACCTGTTTAAATTTACAAAAGCTTGGCT 546
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Db 489 TATGGAATCCATAGGAATACATGAGAGACCTGTTTAAATTTACAAAAGCTTGGCT 548
| | | | |
QY 547 TACACATAGTGAATAATCATCACTATATGATAGTCAATTTTGTCAAGCGCTGGCTG 606
| | | | |
Db 549 TACACATAGTGAATAATCATCACTATATGATAGTCAATTTTGTCAAGCGCTGGCTG 608
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QY 607 ATTCTGTGGTCTTCCAGGTCCTTCATCATTTATGTTGATGAGAGAACTACCCACTCT 666
| | | | |
Db 609 ATTCTGTGGTCTTCCAGGTCCTTCATCATTTATGTTGATGAGAGAACTACCCACTCT 668
| | | | |
QY 667 TTACTATCCACAGAGATCTGGGCTCAGCTGAGTGAATAAATCTATTTTAAAGGGTCTATC 726
| | | | |
Db 669 TTACTATCCACAGAGATCTGGGCTCAGCTGAGTGAATAAATCTATTTTAAAGGGTCTATC 728
| | | | |
QY 727 CTGTGTGTTTCTTCCCTACAGATCTTATGAGATCTATTAATGATGTTGAGAGCAT 786
| | | | |
Db 729 CTGTGTGTTTCTTCCCTACAGATCTTATGAGATCTATTAATGATGTTGAGAGCAT 788
| | | | |
QY 787 TCCAAATGCTGTGACGAGAAAGTTGCAATTTATACGAAATCTTCTTGAAGTGAACGCA 846
| | | | |
Db 789 TCCAAATGCTGTGACGAGAAAGTTGCAATTTATACGAAATCTTCTTGAAGTGAACGCA 848
| | | | |
QY 847 ATTAGCTGCTATGATTTGCTCTCTTGTCTGGGGGAAAGCAATGGTTTAAAGCAAAAG 906
| | | | |
Db 849 ATTAGCTGCTATGATTTGCTCTCTTGTCTGGGGGAAAGCAATGGTTTAAAGCAAAAG 908
| | | | |
QY 907 ATTAATGGCTTATGAAATGTGTGTTTGGCCGT 939
| | | | |
Db 909 ATTAATGGCTTATGAAATGTGTGTTTGGCCGT 941
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RESULT 7
US-10-467-492A-81
; Sequence 81, Application US/10467492A
; Publication No. US2005006976A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: Novel G Protein Coupled Receptor
; FILE REFERENCE: 0411PHEM313
; CURRENT APPLICATION NUMBER: US/10/467,492A
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-467-492A-81

Query Match 98.8%; Score 928.2; DB 21; Length 2525;
Best Local Similarity 99.7%; Pred. No. 3.2e-267;
Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 AAATGTGACTTCCCAAGTATGCTGGGCAACAATACCTCCAGAAATCTCTTGCATTCCT 66
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Db 9 AAGAGTGACTTCCCAAGTATGCTGGGCAACAATACCTCCAGAAATCTCTTGCATTCCT 68
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QY 67 ATAGTACACCCCACTTAATCAAGCTCTACTCATAGTGTCTTAATGAGCGGCTGATGGGT 126
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Db 69 ATAGTACACCCCACTTAATCAAGCTCTACTCATAGTGTCTTAATGAGCGGCTGATGGGT 128
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QY 127 GTCAATTCATCTTTTCTCTCTGGTGAATAAGAACACCCGGTCACTGACACACATGGG 186
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Db 129 GTCAATTCATCTTTTCTCTCTGGTGAATAAGAACACCCGGTCACTGACACACATGGG 188
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QY 187 GTCAATTCATCTTTTCTCTCTGGTGAATAAGAACACCCGGTCACTGACACACATGGG 246
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Db 189 GTCAATTCATCTTTTCTCTCTGGTGAATAAGAACACCCGGTCACTGACACACATGGG 248
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QY 247 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGCCCTTCTGCAAAATTTGATGATG 306
| | | | |
Db 249 TACCTCATCAAGAAAGCTTGAATGTTGGGCTGCCCTTCTGCAAAATTTGATGATG 308
| | | | |
QY 307 CTGCAATCCACATGATACCTCAAGCTTCTATCTATGATGATGATCTGATCAACAGATAC 366
| | | | |
Db 309 CTGCAATCCACATGATACCTCAAGCTTCTATCTATGATGATGATCTGATCAACAGATAC 368
| | | | |
QY 367 CTCATCTTCTTCAAGTCAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGGGCT 426
| | | | |
Db 369 CTCATCTTCTTCAAGTCAGAAAGCAAAAGTGAATTCACAGAAAATGCGTGGGCT 428
| | | | |
QY 427 GCCAGTCTGGCAGATGAGACGCTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCG 486
| | | | |
Db 429 GCCAGTCTGGCAGATGAGACGCTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCG 488
| | | | |
QY 487 TATGGAATCCATAGGAATACATGAGAGACCTGTTTAAATTTACAAAAGCTTGGCT 546
| | | | |
Db 489 TATGGAATCCATAGGAATACATGAGAGACCTGTTTAAATTTACAAAAGCTTGGCT 548
| | | | |
QY 547 TACACATAGTGAATAATCATCACTATATGATAGTCAATTTTGTCAAGCGCTGGCTG 606
| | | | |
Db 549 TACACATAGTGAATAATCATCACTATATGATAGTCAATTTTGTCAAGCGCTGGCTG 608
| | | | |
QY 607 ATTCTGTGGTCTTCCAGGTCCTTCATCATTTATGTTGATGAGAGAACTACCCACTCT 666
| | | | |
Db 609 ATTCTGTGGTCTTCCAGGTCCTTCATCATTTATGTTGATGAGAGAACTACCCACTCT 668
| | | | |
QY 667 TTACTATCCACAGAGATCTGGGCTCAGCTGAGTGAATAAATCTATTTTAAAGGGTCTATC 726
| | | | |
Db 669 TTACTATCCACAGAGATCTGGGCTCAGCTGAGTGAATAAATCTATTTTAAAGGGTCTATC 728
| | | | |
QY 727 CTGTGTGTTTCTTCCCTACAGATCTTATGAGATCTATTAATGATGTTGAGAGCAT 786
| | | | |
Db 729 CTGTGTGTTTCTTCCCTACAGATCTTATGAGATCTATTAATGATGTTGAGAGCAT 788
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QY 787 TCCAAATGCTGTGACGAGAAAGTTGCAATTTATACGAAATCTTCTTGAAGTGAACGCA 846
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Db 789 TCCAAATGCTGTGACGAGAAAGTTGCAATTTATACGAAATCTTCTTGAAGTGAACGCA 848
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QY 847 ATTAGCTGCTATGATTTGCTCTCTTGTCTGGGGGAAAGCAATGGTTTAAAGCAAAAG 906
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Db 849 ATTAGCTGCTATGATTTGCTCTCTTGTCTGGGGGAAAGCAATGGTTTAAAGCAAAAG 908
| | | | |
QY 907 ATTAATGGCTTATGAAATGTGTGTTTGGCCGT 939
| | | | |
Db 909 ATTAATGGCTTATGAAATGTGTGTTTGGCCGT 941
| | | | |

RESULT 8
US-10-975-979-81
; Sequence 81, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Scheinin, Kathleen
; APPLICANT: Bannigan, Chris
; APPLICANT: Ruff, Valerie

APPLICANT: Kaytee, Paul
APPLICANT: Wood, Linda
APPLICANT: Parodi, Luis
APPLICANT: Hiebsch, Ronald
TITLE OF INVENTION: Novel G Protein Coupled Receptors
FILE REFERENCE: 00431PHR293
CURRENT APPLICATION NUMBER: US/10/975,979
CURRENT FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: US/09/714,449
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn version 3.0
SEQ ID NO 81
LENGTH: 2525
TYPE: DNA
ORGANISM: Homo sapiens
US-10-975-979-81

Query Match 98.8%; Score 928.2; DB 21; Length 2525;
Best Local Similarity 99.7%; Pred. No. 3.2e-267;

Matches 930; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 AATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 66
9 ACAGGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 68
67 ATAGTACACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTT 126
69 ATAGTACACCCCACTTAATCACTTCACTTCACTTCACTTCACTTCACTTCACTT 128
127 GTGATTTCCATTTTTCCTCCCTGCTGTAATAATGAACACCCGGTCACTGACCACTATGCG 186
129 GTGATTTCCATTTTTCCTCCCTGCTGTAATAATGAACACCCGGTCACTGACCACTATGCG 188
187 GTGATTTCCATTTTTCCTCCCTGCTGTAATAATGAACACCCGGTCACTGACCACTATGCG 246
189 GTGATTTCCATTTTTCCTCCCTGCTGTAATAATGAACACCCGGTCACTGACCACTATGCG 248
247 TACCTCATCAAGAAAGCTTGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATG 306
249 TACCTCATCAAGAAAGCTTGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATG 308
307 CTGCAATCCACATGTAATCTCAAGCTTCTATTTCTATGTAATGTAATCTGCTGCTGCTGCT 366
309 CTGCAATCCACATGTAATCTCAAGCTTCTATTTCTATGTAATGTAATCTGCTGCTGCTGCT 368
367 CTGATCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGCTGCT 426
369 CTGATCTTCTTCAAGTGAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGCTGCT 428
427 GCCAGTGTGGCATGTGAGCGCTGTGATTTGTCAATGTGTGATGCTGCTGCTGCTGCT 486
429 GCCAGTGTGGCATGTGAGCGCTGTGATTTGTCAATGTGTGATGCTGCTGCTGCTGCT 488

487 TATGATTCATGAGGAAATCAATGAGAGCACTGTTTAAATTTCAAAAGACTTGTCT 546
489 TATGATTCATGAGGAAATCAATGAGAGCACTGTTTAAATTTCAAAAGACTTGTCT 548
547 TACATATGTGAAATATCATCAATATGATATGATATTTTGTCAATGCTGCTGCTG 606
549 TACATATGTGAAATATCATCAATATGATATGATATTTTGTCAATGCTGCTGCTG 608
607 ATTCTGTGCTCTTCCAGGCTTCAATATGATATGATATTTTGTCAATGCTGCTGCT 666
609 ATTCTGTGCTCTTCCAGGCTTCAATATGATATGATATTTTGTCAATGCTGCTGCT 668
667 TTACTATCCACAGGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 726
669 TTACTATCCACAGGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 728
727 CTGTTGTTTCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 786
729 CTGTTGTTTCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAG 788
787 TCCATATGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 846
789 TCCATATGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 848
847 ATTAGGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 906
849 ATTAGGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 908
907 ATATGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 939
909 ATATGCTGTAAGCAAGGCTTCAATTTATTAAGAAATCTTCTTGAAGTGAACGA 941

RESULT 9

US-10-017-161-1193
Sequence 1193, Application US/10017161
Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1193
LENGTH: 1318
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: source
LOCATION: (1)..(1318)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(1118)
US-10-017-161-1193

Query Match 98.8%; Score 927.8; DB 15; Length 1318;
Best Local Similarity 99.8%; Pred. No. 2.8e-267;

Matches 929; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

9 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 68
185 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 244
69 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 128
245 ATGTGACTTCCCAAGTATGCTGGCCACATATCTCCAGAAATCTCTGCGATCT 304


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APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pridie, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIORITY APPLICATION NUMBER: 09/170,496
PRIORITY FILING DATE: 1998-10-13
PRIORITY APPLICATION NUMBER: PCT/US99/23938
PRIORITY FILING DATE: 1998-10-13
PRIORITY APPLICATION NUMBER: 60/253,404
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/255,366
PRIORITY FILING DATE: 2000-12-12
PRIORITY APPLICATION NUMBER: 60/270,286
PRIORITY FILING DATE: 2001-02-20
PRIORITY APPLICATION NUMBER: 60/282,365
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/270,266
PRIORITY FILING DATE: 2001-02-20
PRIORITY APPLICATION NUMBER: 60/282,032
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/282,358
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/282,356
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/290,917
PRIORITY FILING DATE: 2001-05-14
PRIORITY APPLICATION NUMBER: 60/309,208
PRIORITY FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 918
TYPE: DNA
ORGANISM: Homo sapiens
US-09-995-225-3

Query Match      97.3%; Score 913.4; DB 10; Length 918;
Best Local Similarity 99.9%; Pred. No. 4,8e-263;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATGCGTGGCCACATATCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 84
DB 1 ATGCGTGGCCACATATCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 60

QY 85 ATCAGCCTCTACTTCAATGAGTCTTATTTGGGGGCTGGTGGTGTCAATTCATTTCTTTTC 144
DB 61 ATCAGCCTCTACTTCAATGAGTCTTATTTGGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120

QY 145 CTCCTGGTGAATAATGAACACCCGGTCAATGACCAACATGGGGGTCATTAACTTGGTGTG 204
DB 121 CTCCTGGTGAATAATGAACACCCGGTCAATGACCAACATGGGGGTCATTAACTTGGTGTG 180

QY 205 GTCACAGCGCTTTTCTGCTGACAGTGCATTTGCTGTGACCTAATCCTCATCAAGAGACT 264
DB 181 GTCACAGCGCTTTTCTGCTGACAGTGCATTTGCTGTGACCTAATCCTCATCAAGAGACT 240

QY 265 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCAGTATAC 324
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCAGTATAC 300

QY 325 CTCACGTTCTATTTCTATGATGATCTGATGACCAAGATACCTCATCTTCAAGTGC 384
DB 301 CTCACGTTCTATTTCTATGATGATCTGATGACCAAGATACCTCATCTTCAAGTGC 360

QY 385 AAAGACAAAGTGAATTTCTACAGAAACATGATGCTGTGCTGCAGATGCTGCAGATGTG 444
DB 361 AAAGACAAAGTGAATTTCTACAGAAACATGATGCTGTGCTGCAGATGCTGCAGATGTG 420
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QY 445 ACCGTGATATGTCATTTGGGTAACCCCTGTTGTTCTCCGGATGGAATTCATGAGAA 504
DB 421 ACCGTGATATGTCATTTGGGTAACCCCTGTTGTTCTCCGGATGGAATTCATGAGAA 480

QY 505 TACAAATGAGAGACAGCTTTTAAATTTCAAAAGAGCTTCTTACATATGTAATTC 564
DB 481 TACAAATGAGAGACAGCTTTTAAATTTCAAAAGAGCTTCTTACATATGTAATTC 540

QY 565 ATCAACTATATGATATGATCTTTTGTGATAGCCGTTGCTGTGATTTGTTGGTCTTCCAG 624
DB 541 ATCAACTATATGATATGATCTTTTGTGATAGCCGTTGCTGTGATTTGTTGGTCTTCCAG 600

QY 625 GTCCTATCATATATGTTGATGAGGAGAGAGTACAGCAGCATCTTACTATCCACAGAG 684
DB 601 GTCCTATCATATATGTTGATGAGGAGAGAGTACAGCAGCATCTTACTATCCACAGAG 660

QY 685 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTGTTGTTTCTTCC 744
DB 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTGTTGTTTCTTCC 720

QY 745 TACCACTCTTTAGATCTATTACTTGAATGTTGTGACGATTCATGCTGTAGAC 804
DB 721 TACCACTCTTTAGATCTATTACTTGAATGTTGTGACGATTCATGCTGTAGAC 780

QY 805 AAGGTGCAATTTTATAGGAATCTTGAAGTGAACAGCAATTAGCTGATGATTTG 864
DB 781 AAGGTGCAATTTTATAGGAATCTTGAAGTGAACAGCAATTAGCTGATGATTTG 840

QY 865 CTTCCTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAATTTGCTTATGAAAT 924
DB 841 CTTCCTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAATTTGCTTATGAAAT 900

QY 925 TGTGTTTGTGCGGT 939
DB 901 TGTGTTTGTGCGGT 915

RESULT 13
US-10-055-106C-1
Sequence 1, Application US/10055106C
Publication No. US20030017536A1
GENERAL INFORMATION:
APPLICANT: Harland, Lee
TITLE OF INVENTION: Novel Polypeptide
FILE REFERENCE: PC10970AGLK
CURRENT APPLICATION NUMBER: US/10/055,106C
CURRENT FILING DATE: 2002-01-23
PRIORITY APPLICATION NUMBER: GB0101739.1
PRIORITY FILING DATE: 2001-01-23
PRIORITY APPLICATION NUMBER: US 60/267,341
PRIORITY FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 918
TYPE: DNA
ORGANISM: Homo sapiens
US-10-055-106C-1

Query Match      97.3%; Score 913.4; DB 14; Length 918;
Best Local Similarity 99.9%; Pred. No. 4,8e-263;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATGCGTGGCCACATATCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 84
DB 1 ATGCGTGGCCACATATCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 60

QY 85 ATCAGCCTCTACTTCAATGAGTCTTATTTGGGGGCTGGTGGTGTCAATTCATTTCTTTTC 144
DB 61 ATCAGCCTCTACTTCAATGAGTCTTATTTGGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120
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Db      841 CTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTAGGAAT 900
QY      925 TGTGTTTTGTGCCGT 939
Db      901 TGTGTTTTGTGCCGT 915

RESULT 15
US-10-297-908A-2
; Sequence 2, Application US/10297908A
; Publication No. US20040029793A1
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Takeo
; APPLICANT: ITO, Takahashi
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: MIYAJIMA, No. US20040029793A1uyuki
; TITLE OF INVENTION: No. US20040029793A1el G Protein-Coupled Receptor Protein and its
; FILE REFERENCE: 2737 USOP
; CURRENT APPLICATION NUMBER: US/10/297,908A
; PRIOR FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: PCT/JP01/05061
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: JP 2000-184596
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: JP 2000-223887
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Human
US-10-297-908A-2

Query Match      97.3%; Score 913.4; DB 17; Length 918;
Best Local Similarity 99.9%; Pred. No. 4.8e-263;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      25 ATGCTGGGCAACAATACCTCCAGGAATTCCTTTGCGATCTTATAGTACACCCCACTTA 84
Db      1 ATGCTGGGCAACAATACCTCCAGGAATTCCTTTGCGATCTTATAGTACACCCCACTTA 60

QY      85 ATCAGCCTTACTTCAATAGTGCCTTATTTGCGGGCTGGTGGGTGTCAATTTTCATTTCTTTTC 144
Db      61 ATCAGCCTTACTTCAATAGTGCCTTATTTGCGGGCTGGTGGGTGTCAATTTTCATTTCTTTTC 120

QY      145 CTCTGTGTGAAATGAACACCCGGTCAAGTACCAACCATGGCGGTCAATTACTTGGTGTG 204
Db      121 CTCTGTGTGAAATGAACACCCGGTCAAGTACCAACCATGGCGGTCAATTACTTGGTGTG 180

QY      205 GTCACAGCGTTTTTCTGTGACAGTGCATTTGCTTGAACCTTACCTCATCAAGAAAGACT 264
Db      181 GTCACAGCGTTTTTCTGTGACAGTGCATTTGCTTGAACCTTACCTCATCAAGAAAGACT 240

QY      265 TGAATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATGCTGACATCAATGTAC 324
Db      241 TGAATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATGCTGACATCAATGTAC 300

QY      325 CTGACGTTCTATTCTATGTGTGTGATGCTGTGACACGATACCTCAATCTTCAAGTGC 384
Db      301 CTGACGTTCTATTCTATGTGTGTGATGCTGTGACACGATACCTCAATCTTCAAGTGC 360

QY      385 AAAGACAAGTGAATCTACAGAAAATGCTGATGCTGCTGACAGTGCATGTG 444
Db      361 AAAGACAAGTGAATCTACAGAAAATGCTGATGCTGCTGACAGTGCATGTG 420

QY      445 ACCGTGTGATGTGATGTGTGTAACCCGTGTTGTCTCCGGTATGGAATCCATGAGAA 504
Db      421 ACCGTGTGATGTGATGTGTGTAACCCGTGTTGTCTCCGGTATGGAATCCATGAGAA 480

QY      505 TACAATGAGAGACATGTTTAAATTTCAAAAGAGTTTGTCTTACATATGTGAAAATC 564
Db      481 TACAATGAGAGACATGTTTAAATTTCAAAAGAGTTTGTCTTACATATGTGAAAATC 540
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QY      565 ATCAACTATATAGTATGTCATTTTGTGCATAGCCGTGTGATGATTCGTGTGCTTCCAG 624
Db      541 ATCAACTATATAGTATGTCATTTTGTGCATAGCCGTGTGATGATTCGTGTGCTTCCAG 600

QY      625 GTCTTCATCATTAATGTGTGATGTGACAGAAAGTACAGCACTCTTTACTATATCCACAGAG 684
Db      601 GTCTTCATCATTAATGTGTGATGTGACAGAAAGTACAGCACTCTTTACTATATCCACAGAG 660

QY      685 TTCTGGGCTCAGCTGAAAACCTATTTTATATAGGGGTATCCTGTGTGTTCTCTCC 744
Db      661 TTCTGGGCTCAGCTGAAAACCTATTTTATATAGGGGTATCCTGTGTGTTCTCTCC 720

QY      745 TACAGTCTTATAGATCTATTACTTGAATGTGTGACGCAATCCATGCTGTAGCAGC 804
Db      721 TACAGTCTTATAGATCTATTACTTGAATGTGTGACGCAATCCATGCTGTAGCAGC 780

QY      805 AAGTTGCATTTTATTAAGAAAATCTTCTTGAAGTGAACAGCAATTAAGTGTATGATTTG 864
Db      781 AAGTTGCATTTTATTAAGAAAATCTTCTTGAAGTGAACAGCAATTAAGTGTATGATTTG 840

QY      865 CTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATGGCTTAGGAAT 924
Db      841 CTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATGGCTTAGGAAT 900

QY      925 TGTGTTTTGTGCCGT 939
Db      901 TGTGTTTTGTGCCGT 915
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Job time : 679.311 secs